

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 24, 2004, 13:07:03 ; Search time 100.009 Seconds
(without alignments)
2909.975 Million cell updates/sec

Title: US-09-856-681A-2
Perfect score: 5450
Sequence: 1 MRSEALLLYFTLLHFAGAGF.....PPKPSFAPLSTSMKPNDACT 1030

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	5450	100.0	1030	3	AAY71460	Aay71460 Human sem
2	5371.5	98.6	1047	6	ADA23362	Ada23362 Human SEC
3	5103.5	93.6	975	4	AAB90731	Aab90731 Human CJ1
4	5088	93.4	974	2	AAW64221	Aaw64221 Human sec
5	4921	90.3	939	3	AAB23030	Aab23030 Human sem
6	4921	90.3	939	6	ADA23281	Ada23281 Human SEC
7	4590.5	84.2	884	3	AAB23031	Aab23031 Human sem
8	4590.5	84.2	884	6	ADA23283	Ada23283 Human SEC
9	3677	67.5	699	4	AAB95139	Aab95139 Human pro

10	3373	61.9	630	3	AAB23043	Aab23043	Human	sem
11	3373	61.9	630	6	ADA23307	Ada23307	Human	SEC
12	3362	61.7	626	6	ADA23360	Ada23360	Human	SEC
13	2980.5	54.7	574	4	AAB95317	Aab95317	Human	pro
14	2952	54.2	562	4	AAB94104	Aab94104	Human	pro
15	2947	54.1	562	4	AAM93444	Aam93444	Human	pol
16	2891	53.0	863	4	ABG04066	Abg04066	Novel	hum
17	2879.5	52.8	962	4	ABG04620	Abg04620	Novel	hum
18	2621.5	48.1	507	4	AAB92688	Aab92688	Human	pro
19	2361.5	43.3	1086	4	AAG63213	Aag63213	Amino	aci
20	2349.5	43.1	1088	5	ABG79177	Abg79177	Human	sem
21	2346	43.0	1017	5	AAG79413	Aag79413	CADHP-2,	
22	2335	42.8	1035	5	ABG79173	Abg79173	Human	sem
23	2326.5	42.7	1032	5	ABG79175	Abg79175	Human	sem
24	2213	40.6	418	4	AAB95886	Aab95886	Human	pro
25	2013.5	36.9	888	2	AAW19857	Aaw19857	Human	sem
26	2009.5	36.9	888	3	AAB18916	Aab18916	A novel	p
27	2009.5	36.9	888	4	AAU12443	Aau12443	Human	PRO
28	2009.5	36.9	888	5	ABB84950	Abb84950	Human	PRO
29	2009.5	36.9	888	5	ABB95556	Abb95556	Human	ang
30	2009.5	36.9	888	6	ABO17887	Abo17887	Novel	hum
31	2009.5	36.9	888	6	ABU69110	Abu69110	Human	PRO
32	2009.5	36.9	888	6	ABU81141	Abu81141	Human	PRO
33	2009.5	36.9	888	6	ABO19426	Abo19426	Human	sec
34	2009.5	36.9	888	6	ABU66841	Abu66841	Human	PRO
35	2009.5	36.9	888	6	ABU59922	Abu59922	Novel	sec
36	2009.5	36.9	888	6	ABU69087	Abu69087	Human	PRO
37	2009.5	36.9	888	6	ABO25112	Abo25112	Human	sec
38	2009.5	36.9	888	6	ABU67117	Abu67117	Human	sec
39	2009.5	36.9	888	6	ABU81551	Abu81551	Human	sec
40	2009.5	36.9	888	6	ADA46063	Ada46063	Novel	hum
41	2009.5	36.9	888	6	ADA76560	Ada76560	Novel	hum
42	2009.5	36.9	888	6	ADA76494	Ada76494	Human	PRO
43	2009.5	36.9	888	6	ADA19144	Ada19144	Human	PRO
44	2009.5	36.9	888	6	ADA61767	Ada61767	Homo sapi	
45	2009.5	36.9	888	6	ADB19552	Adb19552	Novel	hum

ALIGNMENTS

RESULT 1

AAAY71460

ID AAY71460 standard; protein; 1030 AA.

XX

AC AAY71460;

XX

DT 04-OCT-2000 (first entry)

XX

DE Human semaphorin 6A-1.

XX

KW Human; semaphorin 6A-1; (HSA)SEMA6A-1; neuronal development; apoptosis;

KW neuronal regeneration; Ena/VASP protein family; immunomodulatory;

KW gene therapy; diagnostic agent; therapeutic agent; differentiation;

KW cytoskeletal stabilisation; plasticity.

XX

OS Homo sapiens.

```

XX      Key                Location/Qualifiers
FH      Binding-site      957. .961
FT                                     /note= "Specific binding motif for members of Ena/VASP
FT                                     protein family, especially Evl"
FT      Binding-site      959. .1030
FT                                     /note= "Zyxin-like domain that selectively binds to
FT                                     members of Ena/VASP protein family, especially Evl"
FT      Binding-site      1009. .1014
FT                                     /note= "Specific binding motif for members of Ena/VASP
FT                                     protein family, especially Evl"
XX
PN      WO200031252-A1.
XX
PD      02-JUN-2000.
XX
PF      26-NOV-1999;      99WO-EP009215.
XX
PR      26-NOV-1998;      98EP-00122441.
XX
PA      (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
XX
PI      Behl C,  Klostermann A;
XX
DR      WPI; 2000-400065/34.
DR      N-PSDB; AAD01233.
XX
PT      Nucleic acid coding for human semaphorin 6A-1 used as diagnostic agent,
PT      therapeutic agent, for modulating immune system, in gene therapy or for
PT      effecting differentiation, cytoskeletal stabilization and/or plasticity.
XX
PS      Example 1; Page 29-33; 53pp; English.
XX
CC      The present sequence is a transmembranous human semaphorin 6A-1
CC      ((HSA)SEMA6A-1) which is involved in neuronal development and
CC      regeneration mechanisms during apoptosis. Semaphorin is a family of
CC      proteins displaying secreted or transmembrane-based repulsive guidance
CC      cues critically involved in neuronal development. The present sequence
CC      was isolated from human 1-ZAP Express cDNA library which was screened
CC      using a PCR fragment amplified from human neuroblastoma cell line SK-N-MC
CC      cDNA. The (HSA)SEMA6A-1 protein contains a Zyxin-like domain that
CC      selectively binds to members of Ena/VASP protein family especially Evl.
CC      Expression of (HSA)SEMA6A-1 is highest in embryonic brain and kidney and
CC      moderate in lung. The present sequence is useful as diagnostic and
CC      therapeutic agents, for modulating the immune system, in gene therapy,
CC      for effecting differentiation, cytoskeletal stabilisation and plasticity
XX
SQ      Sequence 1030 AA;

Query Match                100.0%;  Score 5450;  DB 3;  Length 1030;
Best Local Similarity      100.0%;  Pred. No. 0;
Matches 1030;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

Qy      1 MRSEALLLYFTLLHFAGAGFPEDSEPI SISHGNYTKQYPVFVGHKPGRNTTQRHRLDIQM 60
      |||
Db      1 MRSEALLLYFTLLHFAGAGFPEDSEPI SISHGNYTKQYPVFVGHKPGRNTTORHRLDIOM 60

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Qy	61	IMIMNGTLYIAARDHIYTVDIDTSHTEEIYCSKKLTWKSQADVDTCRMKGKHKDECHNF	120
Db	61	IMIMNGTLYIAARDHIYTVDIDTSHTEEIYCSKKLTWKSQADVDTCRMKGKHKDECHNF	120
Qy	121	IKVLLKKND DALFVCGTNAFNPSCRNYKMDTLEPF GDEFSGMARCPYDAKHANVALFADG	180
Db	121	IKVLLKKND DALFVCGTNAFNPSCRNYKMDTLEPF GDEFSGMARCPYDAKHANVALFADG	180
Qy	181	KLYSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYFFFREIA	240
Db	181	KLYSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYFFFREIA	240
Qy	241	VEYNTMGKVVFPRVAQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDSHFYFNILQAVT	300
Db	241	VEYNTMGKVVFPRVAQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDSHFYFNILQAVT	300
Qy	301	DVIRINGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVPDER	360
Db	301	DVIRINGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVPDER	360
Qy	361	VPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRRL	420
Db	361	VPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRRL	420
Qy	421	TKIAVDTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLNDSLFLEEMSVYNSEKCSYD	480
Db	421	TKIAVDTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLNDSLFLEEMSVYNSEKCSYD	480
Qy	481	GVEDKRIMGMLDRASSSLYVAFSTCVIKVPLGRCERHGKCKKTCIASRDPYCGWKEGG	540
Db	481	GVEDKRIMGMLDRASSSLYVAFSTCVIKVPLGRCERHGKCKKTCIASRDPYCGWKEGG	540
Qy	541	ACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALNGHSSSLLPSTTTSDSTAQEGYESR	600
Db	541	ACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALNGHSSSLLPSTTTSDSTAQEGYESR	600
Qy	601	GGMLDWKHL LDSPDSTDPLGAVSSH NHQDKKGVIRESYLKGHDQLVPVTL LAIAVILAFV	660
Db	601	GGMLDWKHL LDSPDSTDPLGAVSSH NHQDKKGVIRESYLKGHDQLVPVTL LAIAVILAFV	660
Qy	661	MGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRGSMSSVTKL SGLFGDTQSKDPKPE	720
Db	661	MGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRGSMSSVTKL SGLFGDTQSKDPKPE	720
Qy	721	AILTPLMHNGKLATPGNTAKMLIKADQHHLDTALPTPESTPTLQQKRKPSRGSREWERN	780
Db	721	AILTPLMHNGKLATPGNTAKMLIKADQHHLDTALPTPESTPTLQQKRKPSRGSREWERN	780
Qy	781	QNLINACTKDMPPMGSPVIPTDLPLRASPSHIPSVVVLPI TQQGYQHEYVDQPKMSEVAQ	840
Db	781	QNLINACTKDMPPMGSPVIPTDLPLRASPSHIPSVVVLPI TQQGYQHEYVDQPKMSEVAQ	840
Qy	841	MALEDQAATLEYKTIKEHLSSKSPNHGVNLVENLDSLPPKVPQREASLGPPGASLSQTGL	900
Db	841	MALEDQAATLEYKTIKEHLSSKSPNHGVNLVENLDSLPPKVPQREASLGPPGASLSQTGL	900
Qy	901	SKRLEMHHSSSYGV DYKRSYPTNSLTRSHQATTLKRNTN SSNSSHL SRNQSFGRGDNPP	960


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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      901 SKRLEMHSSSYGVDYKRSYPTNSLTRSHQATTLKRNNTNSSNSSHLSRNQSFGRGDNPP 960
Qy      961 PAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRTPSLKPDPVPPKPSFAPLS 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      961 PAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRTPSLKPDPVPPKPSFAPLS 1020
Qy      1021 TSMKPNDACT 1030
          ||||||||||
Db      1021 TSMKPNDACT 1030

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RESULT 2

ADA23362

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ID  ADA23362 standard; protein; 1047 AA.
XX
AC  ADA23362;
XX
DT  20-NOV-2003 (first entry)
XX
DE  Human SECX polypeptide, SEC15.
XX
KW  Human; secreted polypeptide; membrane-associated polypeptide; SECX; SEC1;
KW  SEC2; SEC3; SEC4; SEC5; SEC6; SEC7; SEC8; SEC9; SEC10; SEC11; SEC12;
KW  SEC13; SEC14; SEC15; SECX-associated disorder; lung cancer;
KW  cardiovascular disease; oncology disease; immune disorder;
KW  autoimmune disease; transplant rejection; allergy; AIDS; infections;
KW  inflammatory disorder; arthritis; haematopoietic disorder; skin disorder;
KW  atherosclerosis; restenosis; neurological disease; Alzheimer's disease;
KW  trauma; wounds; spinal cord injury; skeletal disorder; cytostatic;
KW  antiinflammatory; immunosuppressive; anti-HIV; antiarthritic;
KW  antiarteriosclerotic; cardiant; neuroprotective; nootropic; vulnerary;
KW  antiallergic; cardiant; dermatological.
XX
OS  Homo sapiens.
XX
PN  US2003054514-A1.
XX
PD  20-MAR-2003.
XX
PF  19-SEP-2001; 2001US-00957187.
XX
PR  09-MAR-1999; 99US-0123667P.
PR  04-JAN-2000; 2000US-0174485P.
PR  08-MAR-2000; 2000US-00520781.
PR  19-SEP-2000; 2000US-0233798P.
PR  20-SEP-2000; 2000US-0234082P.
XX
PA  (SHIM/) SHIMKETS R A.
PA  (LARO/) LAROCHELLE W J.
XX
PI  Shimkets RA, Larochelle WJ;
XX
DR  WPI; 2003-540616/51.
DR  N-PSDB; ADA23361.
XX
PT  New SECX nucleic acids, useful for treating or diagnosing a disorder

```

PT e.g., lung cancer, cardiovascular and oncology diseases, immune disorder,
PT and autoimmune disease.

XX

PS Claim 12; Page 14; 118pp; English.

XX

CC The present invention relates to the isolation of human secreted or
CC membrane-associated (SECX) polypeptides designated SEC1-SEC15, and the
CC polynucleotide sequences encoding them. Also disclosed is a method for
CC screening for a modulator of activity or latency of SECX. The SECX
CC polypeptide and polynucleotide sequences may be used for treating or
CC preventing SECX-associated disorders such as lung cancer, cardiovascular
CC and oncology diseases, immune disorders, autoimmune diseases, transplant
CC rejection, allergy, AIDS, infections, inflammatory disorders, arthritis,
CC haematopoietic disorders, skin disorders, atherosclerosis, restenosis,
CC neurological diseases (e.g. Alzheimer's disease), trauma, wounds, spinal
CC cord injuries, and skeletal disorders. The present sequence represents a
CC SECX polypeptide of the invention.

XX

SQ Sequence 1047 AA;

Query Match 98.6%; Score 5371.5; DB 6; Length 1047;
Best Local Similarity 97.7%; Pred. No. 0;
Matches 1023; Conservative 0; Mismatches 7; Indels 17; Gaps 1;

```
Qy      1 MRSEALLLYFTLLHFAGAGFPEDSEPISSHGNYSKQYPVFVGHKPGRNNTQRRHRLDIQM 60
          |||
Db      1 MRSEALLLYFTLLHFAGAGFPEDSEPISSHCNYSKQYPVFVGHKPGRNNTQRRHRLDIQM 60

Qy     61 IMIMNGTLYIAARDHIYTVDIDTSHTEEIYCSKKLTWKSQRQADVDTCRMKGKHKDECHNF 120
          |||
Db     61 IMIMNGTLYIAARDHIYTVDIDTSHTEEIYCSKKLTWKSQRQADVDTCRMKGKHKDECHNF 120

Qy    121 IKVLLKKND DALFVCGTNAFNPSCRNYKMDTLEPFGDEFSGMARCPYDAKHANVALFADG 180
          |||
Db    121 IKVLLKKND DALFVCGTNAFNPSCRNYKMDTLEPFGDEFSGMARCPYDAKHANVALFADG 180

Qy    181 KLYSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYFFFREIA 240
          |||
Db    181 KLYSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYFFFREIA 240

Qy    241 VEYNTMGKVVFPRVAQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDSHFYFNILQAVT 300
          |||
Db    241 VEYNTMGKVVFPRVAQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDSHFYFNILQAVT 300

Qy    301 DVIRINGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVPDER 360
          |||
Db    301 DVIRINGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVGTGRFKEQKSPDSTWTPVPDER 360

Qy    361 VPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRL 420
          |||
Db    361 VPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRL 420

Qy    421 TKIAVDTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLNDSLFLEEMSVYNSEKCSYD 480
          |||
Db    421 TKIAVDTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLNDSLFLEEMSVYNSEKCSYD 480

Qy    481 GVEDKRIMGMLDRASSSLYVAFSTCVIKVPLGRGERHKGCKKTCIASRDPYCGWIKEGG 540
```

Db	481	GVEDKRIMGMQLDRASSSLYVAFSTCVIKBPLGRDERHGKCKKTCIASRDPYCGWIKEGG	540
Qy	541	ACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALN-----GHSSSL	583
Db	541	ACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALNDISTFLPDNEMSYNTVYGHSSSL	600
Qy	584	PSTTTSDSTAQEGYESRGGMLDWKHLSDPDSTDPLGAVSSSHNHQDKKGVIRESYLKGH	643
Db	601	PSTTTSDSTAQEGYESRGGMLDWKHLSDPDSTDPLGAVSSSHNHQDKKGVIRESYLKGH	660
Qy	644	QLVPVTLIAIAVILAFVMGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRGSMSSVT	703
Db	661	QLVPVTLIAIAVILAFVMGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRGSMSSVT	720
Qy	704	KLSGLFGDTQSKDPKPEAILTPLMHNGKLATPGNTAKMLIKADQHHLDTALPTPESTPT	763
Db	721	KLSGLFGDTWSKDPKPEAILTPLMHNGKLATPGNTAKMLIKADQHHLDTALPTPESTPT	780
Qy	764	LQQRKPSRGSREWERNQNINACTKDMPPMGSPVIPTDLPLRASPSHIPSVVVLPIITQQ	823
Db	781	LQQRKPSRGSREWERNQNINACTKDMPPMGSPVIPTCLPLRASPSHIPSVVVLPIITQQ	840
Qy	824	GYQHEYVDQPKMSEVAQMALEDQAATLEYKTIKEHLSSKSPNHGVNLVENLDSLPPKVPQ	883
Db	841	BYQHEYVDQPKMSEVAQMALEDQAATLEYKTIKEHLSSKSPNHGVNLVENLDSLPPKVPQ	900
Qy	884	REASLGPPGASLSQTGLSKRLEMHHSSSYGVYKRSYPTNSLTRSHQATTLKRNTNSSN	943
Db	901	REASLGPPGASLSQTGLSKRLEMHHSSSYGVYKRSYPTNSLTRSHQATTLKRNTNSSN	960
Qy	944	SSHLNRNQSFGRGDNPPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRT	1003
Db	961	SSHLNRNQSFGRGDNPPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRT	1020
Qy	1004	PSLKPDPVPPKPSFAPLSTSMKPNDACT	1030
Db	1021	PSLKPDPVPPKPSFAPLSTSMKPNDACT	1047

RESULT 3

AAB90731

ID AAB90731 standard; protein; 975 AA.

XX

AC AAB90731;

XX

DT 07-JUN-2001 (first entry)

XX

DE Human CJ145_1 protein sequence SEQ ID 161.

XX

KW Human; secreted protein; nutrient; cytokine modulator; proliferation;
 KW differentiation; immune system modulator; tissue growth; chemotactic;
 KW haemostatic; thrombolytic; anti-inflammatory; tumour inhibition;
 KW haematopoiesis.

XX

OS Homo sapiens.

XX

PN WO200119988-A1.
 XX
 PD 22-MAR-2001.
 XX
 PF 14-SEP-2000; 2000WO-US025135.
 XX
 PR 17-SEP-1999; 99US-00398829.
 XX
 PA (GEMY) GENETICS INST INC.
 XX
 PI Jacobs K, Mccoy JM, Lavallie ER, Collins-Racie LA, Evans C;
 PI Merberg D, Treacy M, Bowman MR, Spaulding V, Agostino MJ;
 XX
 DR WPI; 2001-244801/25.
 DR N-PSDB; AAF98469.
 XX
 PT Isolated nucleic acids encoding polypeptides, useful for modulating e.g.
 PT cytokine and cell proliferation/differentiation activity, the immune
 PT system and hematopoiesis regulating activity.
 XX
 PS Disclosure; Page 487-490; 557pp; English.
 XX
 CC Human cDNA clones represented in AAF98374 - AAF98489 encode secreted
 CC proteins AAB90667 - AAB90750. The cDNA clones are isolated from various
 CC tissue types, and may be used in the prevention, treatment and diagnosis
 CC of diseases associated with inappropriate protein expression. The
 CC polypeptides and nucleic acids may be used as nutrients or to modulate
 CC cytokine and cell proliferation/differentiation activity and may also be
 CC involved in modulation of the immune system. The cDNA sequences,
 CC proteins, their agonists and/or antagonists exhibit haematopoiesis
 CC regulating activity; tissue growth activity; activin/inhibin activity;
 CC chemotactic/chemokinetic activity; haemostatic and thrombolytic activity;
 CC receptor/ligand activity; anti-inflammatory activity; haematopoiesis
 CC activity; cadherin/tumour suppressor activity; and/or tumour inhibition
 CC activity. Included in the invention are probes represented in AAF98490 -
 CC AAF98572 which are specific for the cDNA clones encoding the secreted
 CC proteins
 XX
 SQ Sequence 975 AA;

Query Match 93.6%; Score 5103.5; DB 4; Length 975;
 Best Local Similarity 94.4%; Pred. No. 0;
 Matches 972; Conservative 0; Mismatches 3; Indels 55; Gaps 1;

Qy 1 MRSEALLLYFTLLHFAGAGFPEDSEPI SISHGNYTKQYPVFVGHKPGRN TTQRHRLDIQM 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1 MRSEALLLYFTLLHFAGAGFPEDSEPI SISHGNYTKQYPVFVGHKPGRN TTQRHRLDIQM 60

 Qy 61 IMIMNGTLYIAARDHIYTV DIDSHT EEEIYCSKKLTWKS RQADVDTCRMKGKHKDECHNF 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 61 IMIMNGTLYIAARDHIYTV DIDSHT EEEIYCSKKLTWKS RQADVDTCRMKGKHKDECHNF 120

 Qy 121 IKVLLKKND DALFVCGTNAFNPS CRNYKMDTLEPFGDEFSGMARCPYDAKHANVALFADG 180
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 121 IKVLLKKND DALFVCGTNAFNPS CRNYKMDTLEPFGDEFSGMARCPYDAKHANVALFADG 180

 Qy 181 KLYSATVTDFLAIDAVIYRSLGESPTLR TVKHDSKWLKEPYFVQAVDYG DYIYFFFREIA 240

Db	181		KLYSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYFFFREIA	240
Qy	241		VEYNTMGKVVFPRVAQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDSHFYFNILQAVT	300
Db	241		VEYNTMGKVVFPRVAQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDSHFYFNILQAVT	300
Qy	301		DVIRINGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVPDER	360
Db	301		DVIRINGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVPDER	360
Qy	361		VPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRL	420
Db	361		VPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRL	420
Qy	421		TKIAVDTAAGPYQNHTVFLGSEKGIILKFLARIGNSGFLNDSLFLEEMSVYNSEKCSYD	480
Db	421		TKIAVDTAAGPYQNHTVFLGSEKGIILKFLARIGNSGFLNDSLFLEEMSVYNSEKCSYD	480
Qy	481		GVEDKRIMGMLDRASSSLYVAFSTCVIKVPLGRGERHGKCKKTCIASRDPYCGWKEGG	540
Db	481		GVEDKRIMGMLDRASSSLYVAFSTCVIKVPLGRGERHGKCKKTCIASRDPYCGWKEGG	540
Qy	541		ACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALNGHSSSLPSTTTSDSTAQEGYESR	600
Db	541		ACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALN-----	576
Qy	601		GGMLDWKHLLDSPDSTDPLGAVSSHNDKKGVIRESYLKGHDQLVPVTLLAIAVILAFV	660
Db	577	-----	-----GVIRESYLKGHDQLVPVTLLAIAVILAFV	605
Qy	661		MGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRGSMSSVTKL SGLFGDTQSKDPKPE	720
Db	606		MGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRGSMSSVTKL SGLFGDTQSKDPKPE	665
Qy	721		AILTPLMHNGKLATPGNTAKMLIKADQHHLDTALPTPESTPTLQQKRKPSRGSREWERN	780
Db	666		AILTPLMHNGKLATPGNTAKMLIKADQHHLDTALPTPESTPTLQQKRKPSRGSREWERN	725
Qy	781		QNLINACTKDMPPMGSPVIPTDLPLRASPSHIPSVVVLPI TQQGYQHEYVDQPKMSEVAQ	840
Db	726		QNLINACTKDMPPMGSPVIPTDLPLRASPSHIPSVVVLPI TQQGYQHEYVDQPKMSEVAQ	785
Qy	841		MALEDQAATLEYKTIKEHLSSKSPNHGVNLVENLDSLPPKVPQREASLGPPGASLSQTGL	900
Db	786		MALEDQAATLEYKTIKEHFSSKSPNHGVNLVENLDSLPPKVPQREASLGPPGASLFQTGL	845
Qy	901		SKRLEMHHSSSYGV DYKRSYPTNSLTRSHQATTLKRNTNSSNSSHL SRNQSFGRGDNPP	960
Db	846		SKRLEMHHSFSYGV DYKRSYPTNSLTRSHQATTLKRNTNSSNSSHL SRNQSFGRGDNPP	905
Qy	961		PAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRTPSLKPDPVPPKPSFAPLS	1020
Db	906		PAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRTPSLKPDPVPPKPSFAPLS	965
Qy	1021		TSMKPNDACT	1030

RESULT 4

AAW64221

ID AAW64221 standard; protein; 974 AA.

XX

AC AAW64221;

XX

DT 06-OCT-1998 (first entry)

XX

DE Human secreted protein from clone CJ145_1.

XX

KW Secreted protein; human fetal brain; nutrition; cytokine; stimulant;
KW cell proliferation; differentiation; immune system; suppressor; ligand;
KW regulator; hematopoiesis; tissue growth; activin; inhibin; haemostatic;
KW chemotaxis; chemokinetic; thrombosis; receptor; cadherin; tumour;
KW anti-inflammatory.

XX

OS Homo sapiens.

XX

PN WO9827205-A2.

XX

PD 25-JUN-1998.

XX

PF 17-DEC-1997; 97WO-US023330.

XX

PR 18-DEC-1996; 96US-00769192.

PR 13-JAN-1997; 97US-00783401.

PR 16-DEC-1997; 97US-00991872.

XX

PA (GEMY) GENETICS INST INC.

XX

PI Jacobs K, Mccoy JM, Lavallie ER, Racie LA, Merberg D, Treacy M;
PI Spaulding V, Agostino MJ;

XX

DR WPI; 1998-362774/31.

DR N-PSDB; AAV44295.

XX

PT New polynucleotides and secreted proteins - obtained from human foetal
PT brain, human adult testes, human adult brain and human adult salivary
PT gland cDNA libraries.

XX

PS Claim 17j; Page 71-74; 110pp; English.

XX

CC This sequence represents a novel secreted protein from clone CJ145_1
CC isolated from a human fetal brain cDNA library. This protein has
CC applications for nutritional use, cytokine and cell
CC proliferation/differentiation activity, immune stimulating or suppressing
CC activity, hematopoiesis regulating activity, tissue growth activity,
CC activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombotic activity, receptor/ligand activity, anti-inflammatory
CC activity, cadherin/tumour invasion suppressor activity, tumour inhibition
CC activity and other activities

XX

SQ Sequence 974 AA;

Query Match 93.4%; Score 5088; DB 2; Length 974;
Best Local Similarity 94.3%; Pred. No. 0;
Matches 971; Conservative 0; Mismatches 3; Indels 56; Gaps 2;

Qy	1	MRSEALLLYFTLLHFAGAGFPEDSEPISISHGNYTKQYPVFVGHKPGRNNTQRHRLDIQM	60
Db	1	MRSEALLLYFTLLHFAGAGFPEDSEPISISHGNYTKQYPVFVGHKPGRNNTQRHRLDIQM	60
Qy	61	IMIMNGTLYIAARDHIYTVDIDTSHTEEIYCSKKLTWKSQRQADVDTCRMKGKHKDECHNF	120
Db	61	IMIMNGTLYIAARDHIYTVDIDTSH-EEIYCSKKLTWKSQRQADVDTCRMKGKHKDECHNF	119
Qy	121	IKVLLKKNDALFVCGTNAFNPSCRNYKMDTLEPFGDEFSGMARCPYDAKHANVALFADG	180
Db	120	IKVLLKKNDALFVCGTNAFNPSCRNYKMDTLEPFGDEFSGMARCPYDAKHANVALFADG	179
Qy	181	KLYSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYFFFREIA	240
Db	180	KLYSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYFFFREIA	239
Qy	241	VEYNTMGKVVFPRVAQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDSHFYFNILQAVT	300
Db	240	VEYNTMGKVVFPRVAQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDSHFYFNILQAVT	299
Qy	301	DVIRINGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVPDER	360
Db	300	DVIRINGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVPDER	359
Qy	361	VPKPRGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRRL	420
Db	360	VPKPRGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRRL	419
Qy	421	TKIAVDTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLNDSLFLEEMSVYNSEKCSYD	480
Db	420	TKIAVDTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLNDSLFLEEMSVYNSEKCSYD	479
Qy	481	GVEDKRIMGMLDRASSSLYVAFSTCVIKVPLGRGERHGKCKKTCIASRDPYCGWKEGG	540
Db	480	GVEDKRIMGMLDRASSSLYVAFSTCVIKVPLGRGERHGKCKKTCIASRDPYCGWKEGG	539
Qy	541	ACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALNGHSSSLLPSTTTSDSTAQEGYESR	600
Db	540	ACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALN-----	575
Qy	601	GGMLDWKHLLDSPDSTDPLGAVSSHNHQDKKGVIRESYLKGHDLVPVTLTLLAIAVILAFV	660
Db	576	-----GVIRESYLKGHDLVPVTLTLLAIAVILAFV	604
Qy	661	MGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRGSMSSVTKLSGLFGDTQSKDPKPE	720
Db	605	MGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRGSMSSVTKLSGLFGDTQSKDPKPE	664
Qy	721	AILTPLMHNGKLATPGNTAKMLIKADQHHLDTALPTPESTPTLQQKRKPSRGSREWERN	780
Db	665	AILTPLMHNGKLATPGNTAKMLIKADQHHLDTALPTPESTPTLQQKRKPSRGSREWERN	724
Qy	781	QNLINACTKDMPPMGSPVIPTDLPLRASPSHIPSVVVLPITQQGYQHEYVDQPKMSEVAQ	840

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      |||
Db      725 QNLINACTKDMPPMGSPVIPTDLPLRASPSHIPSVVVLPIITQQGYQHEYVDQPKMSEVAQ 784
      |||
Qy      841 MALEDQAATLEYKTIKEHLSSKSPNHGVNLVENLDSLPPKVPQREASLGPPGASLSQTGL 900
      |||
Db      785 MALEDQAATLEYKTIKEHFSSKSPNHGVNLVENLDSLPPKVPQREASLGPPGASLFQTGL 844
      |||
Qy      901 SKRLEMHHSSSYGVYKRSYPTNSLTRSHQATTLKRNTNSSNSSHLSRNQSFGRGDNPP 960
      |||
Db      845 SKRLEMHHSFSGYGVYKRSYPTNSLTRSHQATTLKRNTNSSNSSHLSRNQSFGRGDNPP 904
      |||
Qy      961 PAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRTPSLKPDVPPKPSFAPLS 1020
      |||
Db      905 PAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRTPSLKPDVPPKPSFAPLS 964
      |||
Qy      1021 TSMKPNDACT 1030
      |||
Db      965 TSMKPNDACT 974

```

RESULT 5

AAB23030

ID AAB23030 standard; protein; 939 AA.

XX

AC AAB23030;

XX

DT 16-JAN-2001 (first entry)

XX

DE Human semaphorin protein-like splice variant, SECX 2864933-1.

XX

KW SECX protein; human; secreted; membrane-associated; cancer;
KW proliferation regulator; differentiation regulator; non-malignant tumour;
KW immune disorder; autoimmune disease; transplant rejection; allergy; AIDS;
KW infection; inflammatory disorder; arthritis; haematopoietic disorder;
KW skin disorder; cardiovascular disorder; atherosclerosis; restenosis;
KW neurological disease; Alzheimer's disease; trauma; wounding;
KW spinal cord injury; skeletal disorder; cytostatic; immunosuppressive;
KW anti-HIV; antiinflammatory; antiarthritic; antiarteriosclerotic;
KW neuroprotective; vulnerary; antiallergic; antimicrobial; cardiant;
KW dermatological; gene therapy.

XX

OS Homo sapiens.

XX

PN WO200053742-A2.

XX

PD 14-SEP-2000.

XX

PF 09-MAR-2000; 2000WO-US006280.

XX

PR 09-MAR-1999; 99US-0123667P.

PR 08-MAR-2000; 2000US-0520781P.

XX

PA (CURA-) CURAGEN CORP.

XX

PI Shimkets RA;

XX

DR WPI; 2000-594318/56.

DR N-PSDB; AAA93617.

XX

PT Novel human membrane associated or secreted polypeptides and
PT polynucleotides useful for diagnosis, prevention and treatment of
PT pathological states such as cancer, immune, cardiovascular and
PT neurological disorders.

XX

PS Claim 1; Fig 2; 151pp; English.

XX

CC Sequences AAB23029-B23048 represent human SECX proteins. The SECX
CC proteins of the invention are either secreted or membrane-associated
CC proteins and act as regulator of cellular proliferation and
CC differentiation. SECX proteins or nucleotides are useful for diagnosing
CC the presence of, or predisposition to, a disease associated with altered
CC levels of SECX proteins and nucleotides. The SECX proteins are also
CC useful to screen compounds that modulate SECX activity or expression. The
CC interaction of a SECX protein with other cellular proteins may be useful
CC to modulate the activity of a partner protein, cellular proliferation,
CC cellular differentiation and cell survival. SECX nucleotides are useful
CC for the recombinant expression of SECX protein, and may be used detect
CC SECX mRNA or genetic lesions in the SECX gene. They may also be used to
CC modulate SECX expression (e.g., using antisense oligonucleotides). SECX
CC nucleic acid sequences are also useful for identifying a cell or tissue
CC type in a biological sample, and in forensic biology. SECX primers or
CC probes are useful for detecting the presence of SECX nucleotides and for
CC screening tissue cultures for contamination. Diseases that may be treated
CC or prevented using SECX proteins or nucleotides include cancer (e.g.,
CC colorectal carcinoma, prostate cancer), benign tumours, immune disorders
CC (including autoimmune diseases, transplant rejection, allergies, AIDS),
CC infections, inflammatory disorders, arthritis, haematopoietic disorders,
CC skin disorders, cardiovascular disorders, atherosclerosis, restenosis,
CC neurological diseases (e.g., Alzheimer's disease), trauma (e.g., surgical
CC or traumatic wounds, spinal cord injury), and skeletal disorders

XX

SQ Sequence 939 AA;

Query Match 90.3%; Score 4921; DB 3; Length 939;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 928; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MRSEALLLYFTLLHFAGAGFPEDSEPISISHGNYTKQYPVFVGHKPGRNTTQRHRLDIQM 60
|
Db 1 MRSEALLLYFTLLHFAGAGFPEDSEPISISHGNYTKQYPVFVGHKPGRNTTQRHRLDIQM 60

Qy 61 IMIMNGTLYIAARDHIYTVDIDTSHTEEIYCSKKLTWKSQRQADVDTCRMKGKHKDECHNF 120
|
Db 61 IMIMNGTLYIAARDHIYTVDIDTSHTEEIYCSKKLTWKSQRQADVDTCRMKGKHKDECHNF 120

Qy 121 IKVLLKKNDDALFVCGTNAFNPSCRNYKMDTLEPFGDEFSGMARCPYDAKHANVALFADG 180
|
Db 121 IKVLLKKNDDALFVCGTNAFNPSCRNYKMDTLEPFGDEFSGMARCPYDAKHANVALFADG 180

Qy 181 KLYSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYFFFREIA 240
|
Db 181 KLYSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYFFFREIA 240

Qy 241 VEYNTMGKVVFPRVAQVCKNDMGGSQRVLEKQWTSFLKARLNCVPGDSHFYFNILQAVT 300

Db	241	VEYNTMGKVVFPRVAQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDSHFYFNILQAVT	300
Qy	301	DVIRINGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVPDER	360
Db	301	DVIRINGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVPDER	360
Qy	361	VPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRL	420
Db	361	VPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRL	420
Qy	421	TKIAVDTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLNDSLFLEEMSVYNSEKCSYD	480
Db	421	TKIAVDTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLNDSLFLEEMSVYNSEKCSYD	480
Qy	481	GVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRGERHGKCKKTCIASRDPYCGWIKEGG	540
Db	481	GVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRGERHGKCKKTCIASRDPYCGWIKEGG	540
Qy	541	ACSHLSPNSRLTFEQDIERGNTDGLGDCCHNSFVALNGHSSSLPSTTTSDSTAQEGYESR	600
Db	541	ACSHLSPNSRLTFEQDIERGNTDGLGDCCHNSFVALNGHSSSLPSTTTSDSTAQEGYESR	600
Qy	601	GGMLDWKHLLDSPDSTDPLGAVSSHNHQQKKGVIRESYLKGHDQLVPVTLIAIVILAFV	660
Db	601	GGMLDWKHLLDSPDSTDPLGAVSSHNHQQKKGVIRESYLKGHDQLVPVTLIAIVILAFV	660
Qy	661	MGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRGSMSSVTKLSGLFGDTQSKDPKPE	720
Db	661	MGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRGSMSSVTKLSGLFGDTQSKDPKPE	720
Qy	721	AILTPLMHNGKLATPGNTAKMLIKADQHHLDTALPTPESTPTLQQKRKPSRGSREWERN	780
Db	721	AILTPLMHNGKLATPGNTAKMLIKADQHHLDTALPTPESTPTLQQKREPSRGTREWERN	780
Qy	781	QNLINACTKDMPPMGSPVIPTDLPLRASPSHIPSVVVLPIITQQGYQHEYVDQPKMSEVAQ	840
Db	781	QNLINACTKDMPPMGSPVIPTDLPLRASPSHIPSVVVLPIITQQGYQHEYVDQPKMSEVAQ	840
Qy	841	MALEDQAATLEYKTIKEHLSSKSPNHGVNLVENLDSLPPKVPQREASLGPPGASLSQTGL	900
Db	841	MALEDQAATLEYKTIKEHLSSKSPNHGVNLVENLDSLPPKVPQREASLGPPGASLSQTGL	900
Qy	901	SKRLEMHHSSSYGVYKRSYPTNSLTRSHQAT	932
Db	901	SKRLEMHHSSSYGVYKRSYPTNSLTRSHLTT	932

RESULT 6

ADA23281

ID ADA23281 standard; protein; 939 AA.

XX

AC ADA23281;

XX

DT 20-NOV-2003 (first entry)

XX

DE Human SECX polypeptide, SEC2.

XX
 KW Human; secreted polypeptide; membrane-associated polypeptide; SECX; SEC1;
 KW SEC2; SEC3; SEC4; SEC5; SEC6; SEC7; SEC8; SEC9; SEC10; SEC11; SEC12;
 KW SEC13; SEC14; SEC15; SECX-associated disorder; lung cancer;
 KW cardiovascular disease; oncology disease; immune disorder;
 KW autoimmune disease; transplant rejection; allergy; AIDS; infections;
 KW inflammatory disorder; arthritis; haematopoietic disorder; skin disorder;
 KW atherosclerosis; restenosis; neurological disease; Alzheimer's disease;
 KW trauma; wounds; spinal cord injury; skeletal disorder; cytostatic;
 KW antiinflammatory; immunosuppressive; anti-HIV; antiarthritic;
 KW antiarteriosclerotic; cardiant; neuroprotective; nootropic; vulnerary;
 KW antiallergic; cardiant; dermatological.
 XX
 OS Homo sapiens.
 XX
 PN US2003054514-A1.
 XX
 PD 20-MAR-2003.
 XX
 PF 19-SEP-2001; 2001US-00957187.
 XX
 PR 09-MAR-1999; 99US-0123667P.
 PR 04-JAN-2000; 2000US-0174485P.
 PR 08-MAR-2000; 2000US-00520781.
 PR 19-SEP-2000; 2000US-0233798P.
 PR 20-SEP-2000; 2000US-0234082P.
 XX
 PA (SHIM/) SHIMKETS R A.
 PA (LARO/) LAROCHELLE W J.
 XX
 PI Shimkets RA, Larochelle WJ;
 XX
 DR WPI; 2003-540616/51.
 DR N-PSDB; ADA23280.
 XX
 PT New SECX nucleic acids, useful for treating or diagnosing a disorder
 PT e.g., lung cancer, cardiovascular and oncology diseases, immune disorder,
 PT and autoimmune disease.
 XX
 PS Claim 12; Fig 2; 118pp; English.
 XX
 CC The present invention relates to the isolation of human secreted or
 CC membrane-associated (SECX) polypeptides designated SEC1-SEC15, and the
 CC polynucleotide sequences encoding them. Also disclosed is a method for
 CC screening for a modulator of activity or latency of SECX. The SECX
 CC polypeptide and polynucleotide sequences may be used for treating or
 CC preventing SECX-associated disorders such as lung cancer, cardiovascular
 CC and oncology diseases, immune disorders, autoimmune diseases, transplant
 CC rejection, allergy, AIDS, infections, inflammatory disorders, arthritis,
 CC haematopoietic disorders, skin disorders, atherosclerosis, restenosis,
 CC neurological diseases (e.g. Alzheimer's disease), trauma, wounds, spinal
 CC cord injuries, and skeletal disorders. The present sequence represents a
 CC SECX polypeptide of the invention.
 XX
 SQ Sequence 939 AA;

Query Match

90.3%; Score 4921; DB 6; Length 939;

Best Local Similarity 99.6%; Pred. No. 0;
Matches 928; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

```
Qy      1 MRSEALLLYFTLLHFAGAGFPEDSEPISISHGNYTKQYPVFVGHKPGRNTTQRHRLDIQM 60
      |||
Db      1 MRSEALLLYFTLLHFAGAGFPEDSEPISISHGNYTKQYPVFVGHKPGRNTTQRHRLDIQM 60

Qy     61 IMIMNGTLYIAARDHIYTVDIDTSHTEEIYCSKKLTWKSQRQADVDCRMKGKHKDECHNF 120
      |||
Db     61 IMIMNGTLYIAARDHIYTVDIDTSHTEEIYCSKKLTWKSQRQADVDCRMKGKHKDECHNF 120

Qy    121 IKVLLKKND DALFVCGTNAFNPNSCRNYKMDTLEPFGDEFSGMARCPYDAKHANVALFADG 180
      |||
Db    121 IKVLLKKND DALFVCGTNAFNPNSCRNYKMDTLEPFGDEFSGMARCPYDAKHANVALFADG 180

Qy    181 KLYSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYFFFREIA 240
      |||
Db    181 KLYSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYFFFREIA 240

Qy    241 VEYNTMGKVVFPRVAQVCKNDMGGSQRVLEKQWTSFLKARLNCSPGDSHFYFNILQAVT 300
      |||
Db    241 VEYNTMGKVVFPRVAQVCKNDMGGSQRVLEKQWTSFLKARLNCSPGDSHFYFNILQAVT 300

Qy    301 DVIRINGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVPPER 360
      |||
Db    301 DVIRINGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVPPER 360

Qy    361 VPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRL 420
      |||
Db    361 VPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRL 420

Qy    421 TKIAVDTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLNDSLFLEEMSVYNSEKCSYD 480
      |||
Db    421 TKIAVDTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLNDSLFLEEMSVYNSEKCSYD 480

Qy    481 GVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRGERHGKCKKTCIASRDPYCGWIKEGG 540
      |||
Db    481 GVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRGERHGKCKKTCIASRDPYCGWIKEGG 540

Qy    541 ACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALNGHSSSLPSTTTSDSTAQEGYESR 600
      |||
Db    541 ACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALNGHSSSLPSTTTSDSTAQEGYESR 600

Qy    601 GGMLDWKHL DSDPDST DPLGAVSSH NHQDKKGVIRESYLK GHDQLVPV TLLAIAVILAFV 660
      |||
Db    601 GGMLDWKHL DSDPDST DPLGAVSSH NHQDKKGVIRESYLK GHDQLVPV TLLAIAVILAFV 660

Qy    661 MGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRGSMSSSVTKLSGLFGDTQSKDPKPE 720
      |||
Db    661 MGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRGSMSSSVTKLSGLFGDTQSKDPKPE 720

Qy    721 AILTPLMHNGKLATPGNTAKMLIKADQHHLDTALPTPESTPTLQQKRKPSRGSRREWERN 780
      |||
Db    721 AILTPLMHNGKLATPGNTAKMLIKADQHHLDTALPTPESTPTLQQKREPSRGRTREWERN 780

Qy    781 QNLINACTKDMPPMGSPVIPTDLPLRASPSHIPSVVVLPI TQQGYQHEYVDQPKMSEVAQ 840
      |||
```

Db 781 QNLINACTKDMPPMGSPVIPTDLPLRASPSHIPSVVVLPTITQQGYQHEYVDQPKMSEVAQ 840

Qy 841 MALEDQAATLEYKTIKEHLSSKSPNHGVNLVENLDSLPPKVPQREASLGPPGASLSQTGL 900
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 841 MALEDQAATLEYKTIKEHLSSKSPNHGVNLVENLDSLPPKVPQREASLGPPGASLSQTGL 900

Qy 901 SKRLEMHHSSSYGVDYKRSYPTNSLTRSHQAT 932
 |||||||||||||||||||||||||||||

Db 901 SKRLEMHHSSSYGVDYKRSYPTNSLTRSHLTT 932

RESULT 7

AAB23031

ID AAB23031 standard; protein; 884 AA.

XX

AC AAB23031;

XX

DT 16-JAN-2001 (first entry)

XX

DE Human semaphorin protein-like splice variant, SECX 2864933-2.

XX

KW SECX protein; human; secreted; membrane-associated; cancer;
 KW proliferation regulator; differentiation regulator; non-malignant tumour;
 KW immune disorder; autoimmune disease; transplant rejection; allergy; AIDS;
 KW infection; inflammatory disorder; arthritis; haematopoietic disorder;
 KW skin disorder; cardiovascular disorder; atherosclerosis; restenosis;
 KW neurological disease; Alzheimer's disease; trauma; wounding;
 KW spinal cord injury; skeletal disorder; cytostatic; immunosuppressive;
 KW anti-HIV; antiinflammatory; antiarthritic; antiarteriosclerotic;
 KW neuroprotective; vulnerary; antiallergic; antimicrobial; cardiant;
 KW dermatological; gene therapy.

XX

OS Homo sapiens.

XX

PN WO200053742-A2.

XX

PD 14-SEP-2000.

XX

PF 09-MAR-2000; 2000WO-US006280.

XX

PR 09-MAR-1999; 99US-0123667P.

PR 08-MAR-2000; 2000US-0520781P.

XX

PA (CURA-) CURAGEN CORP.

XX

PI Shimkets RA;

XX

DR WPI; 2000-594318/56.

DR N-PSDB; AAA93618.

XX

PT Novel human membrane associated or secreted polypeptides and
 PT polynucleotides useful for diagnosis, prevention and treatment of
 PT pathological states such as cancer, immune, cardiovascular and
 PT neurological disorders.

XX

PS Claim 1; Fig 3; 151pp; English.

XX

CC Sequences AAB23029-B23048 represent human SECX proteins. The SECX
 CC proteins of the invention are either secreted or membrane-associated
 CC proteins and act as regulator of cellular proliferation and
 CC differentiation. SECX proteins or nucleotides are useful for diagnosing
 CC the presence of, or predisposition to, a disease associated with altered
 CC levels of SECX proteins and nucleotides. The SECX proteins are also
 CC useful to screen compounds that modulate SECX activity or expression. The
 CC interaction of a SECX protein with other cellular proteins may be useful
 CC to modulate the activity of a partner protein, cellular proliferation,
 CC cellular differentiation and cell survival. SECX nucleotides are useful
 CC for the recombinant expression of SECX protein, and may be used detect
 CC SECX mRNA or genetic lesions in the SECX gene. They may also be used to
 CC modulate SECX expression (e.g., using antisense oligonucleotides). SECX
 CC nucleic acid sequences are also useful for identifying a cell or tissue
 CC type in a biological sample, and in forensic biology. SECX primers or
 CC probes are useful for detecting the presence of SECX nucleotides and for
 CC screening tissue cultures for contamination. Diseases that may be treated
 CC or prevented using SECX proteins or nucleotides include cancer (e.g.,
 CC colorectal carcinoma, prostate cancer), benign tumours, immune disorders
 CC (including autoimmune diseases, transplant rejection, allergies, AIDS),
 CC infections, inflammatory disorders, arthritis, haematopoietic disorders,
 CC skin disorders, cardiovascular disorders, atherosclerosis, restenosis,
 CC neurological diseases (e.g., Alzheimer's disease), trauma (e.g., surgical
 CC or traumatic wounds, spinal cord injury), and skeletal disorders

XX

SQ Sequence 884 AA;

Query Match 84.2%; Score 4590.5; DB 3; Length 884;
 Best Local Similarity 93.7%; Pred. No. 0;
 Matches 873; Conservative 2; Mismatches 2; Indels 55; Gaps 1;

Qy	1	MRSEALLLYFTLLHFAGAGFPEDSEPI	ISHGNYTKQYPVFVGHKPGRNTTQRHRLDIQM	60
Db	1	MRSEALLLYFTLLHFAGAGFPEDSEPI	ISHGNYTKQYPVFVGHKPGRNTTQRHRLDIQM	60
Qy	61	IMIMNGTLYIAARDHIYTV	DIDTSHTEEIYCSKKLTWKS	RQADV
Db	61	IMIMNGTLYIAARDHIYTV	DIDTSHTEEIYCSKKLTWKS	RQADV
Qy	121	IKVLLKKNDALFVCGTNAFNP	SCRNYKMDTLEPFGDEFSG	MARCPYDAKHANVALFADG
Db	121	IKVLLKKNDALFVCGTNAFNP	SCRNYKMDTLEPFGDEFSG	MARCPYDAKHANVALFADG
Qy	181	KLYSATVTDFLAIDAVIYRSL	GESPTLRTVKHDSKWLKEPYFVQAVDYGDYIYFF	FFREIA
Db	181	KLYSATVTDFLAIDAVIYRSL	GESPTLRTVKHDSKWLKEPYFVQAVDYGDYIYFF	FFREIA
Qy	241	VEYNTMGKVVFP	QVCKNDMGGSQ	RVLKQWTSFLKARLNCSVPGDSHFYFNILQAVT
Db	241	VEYNTMGKVVFP	QVCKNDMGGSQ	RVLKQWTSFLKARLNCSVPGDSHFYFNILQAVT
Qy	301	DVIRINGRDVVLATFSTPYNSIP	GS	SAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVPDER
Db	301	DVIRINGRDVVLATFSTPYNSIP	GS	SAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVPDER
Qy	361	VPKPRPGCCAGSSSLERYATSNEFP	DDTLNFIKTHPLMDEAVPSIFNRPWF	LRTMVR

Db	361	VPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRL	420
Qy	421	TKIAVDTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLNDSLFLEEMSVYNSEKCSYD	480
Db	421	TKIAVDTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLNDSLFLEEMSVYNSEKCSYD	480
Qy	481	GVEDKRIMGMLDRASSSLYVAFSTCVIKVPLGRCERHGKCKKTCIASRDPYCGWIKEGG	540
Db	481	GVEDKRIMGMLDRASSSLYVAFSTCVIKVPLGRCERHGKCKKTCIASRDPYCGWIKEGG	540
Qy	541	ACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALNGHSSSLLPSTTTSDSTAQEGYESR	600
Db	541	ACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALN-----	576
Qy	601	GGMLDWKHLLDSPDSTDPLGAVSSHNDKKGVIRESYLKGHDQLVPVTLTLLAIAVILAFV	660
Db	577	-----GVIRESYLKGHDQLVPVTLTLLAIAVILAFV	605
Qy	661	MGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRGSMSSVTKLSGLFGDTQSKDPKPE	720
Db	606	MGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRGSMSSVTKLSGLFGDTQSKDPKPE	665
Qy	721	AILTPLMHNGKLATPGNTAKMLIKADQHHLDTALPTPESTPTLQQKRKPSRGSREWERN	780
		: : :	
Db	666	AILTPLMHNGKLATPGNTAKMLIKADQHHLDTALPTPESTPTLQQKREPSRGTRREWERN	725
Qy	781	QNLINACTKDMPPMGSPVIPTDLPLRASPSHIPSVVVLPIITQQGYQHEYVDQPKMSEVAQ	840
Db	726	QNLINACTKDMPPMGSPVIPTDLPLRASPSHIPSVVVLPIITQQGYQHEYVDQPKMSEVAQ	785
Qy	841	MALEDQAATLEYKTIKEHLSSKSPNHGVNLVENLDSLPPKVPQREASLGPPGASLSQTGL	900
Db	786	MALEDQAATLEYKTIKEHLSSKSPNHGVNLVENLDSLPPKVPQREASLGPPGASLSQTGL	845
Qy	901	SKRLEMHHSSSYGVVDYKRSYPTNSLTRSHQAT	932
Db	846	SKRLEMHHSSSYGVVDYKRSYPTNSLTRSHLTT	877

RESULT 8

ADA23283

ID ADA23283 standard; protein; 884 AA.

XX

AC ADA23283;

XX

DT 20-NOV-2003 (first entry)

XX

DE Human SECX polypeptide, SEC3 #1.

XX

KW Human; secreted polypeptide; membrane-associated polypeptide; SECX; SEC1;

KW SEC2; SEC3; SEC4; SEC5; SEC6; SEC7; SEC8; SEC9; SEC10; SEC11; SEC12;

KW SEC13; SEC14; SEC15; SECX-associated disorder; lung cancer;

KW cardiovascular disease; oncology disease; immune disorder;

KW autoimmune disease; transplant rejection; allergy; AIDS; infections;

KW inflammatory disorder; arthritis; haematopoietic disorder; skin disorder;

KW atherosclerosis; restenosis; neurological disease; Alzheimer's disease;

KW trauma; wounds; spinal cord injury; skeletal disorder; cytostatic;

Db	61	IMIMNGTLYIAARDHIYTVDIDTSHTEEIYCSKKLTWKSQRQADVDTCRMKGKHKDECHNF	120
Qy	121	IKVLLKKND DALFVCGTNAFNPSCRNYKMDTLEPF GDEFSGMARC PYDAKHANVALFADG	180
Db	121	IKVLLKKND DALFVCGTNAFNPSCRNYKMDTLEPF GDEFSGMARC PYDAKHANVALFADG	180
Qy	181	KLYSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYFFFREIA	240
Db	181	KLYSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYFFFREIA	240
Qy	241	VEYNTMGKVVFPRAVQCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDSHFYFNILQAVT	300
Db	241	VEYNTMGKVVFPRAVQCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDSHFYFNILQAVT	300
Qy	301	DVIRINGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVPDER	360
Db	301	DVIRINGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVPDER	360
Qy	361	VPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFRLRTMVRYRL	420
Db	361	VPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFRLRTMVRYRL	420
Qy	421	TKIAVDTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLNDSL FLEEMSVYNSEKCSYD	480
Db	421	TKIAVDTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLNDSL FLEEMSVYNSEKCSYD	480
Qy	481	GVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGR CERH GKCKKTCIASRDPYCGWIKEGG	540
Db	481	GVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGR CERH GKCKKTCIASRDPYCGWIKEGG	540
Qy	541	ACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALNGHSSSLPSTTTSDSTAQEGYESR	600
Db	541	ACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALN-----	576
Qy	601	GGMLDWKHL L D S P D S T D P L G A V S S H N H Q D K K G V I R E S Y L K G H D Q L V P V T L L A I A V I L A F V	660
Db	577	-----GVIRESYLKGH D Q L V P V T L L A I A V I L A F V	605
Qy	661	MGAVFSGITVYCVCDHRRKDVA V V Q R K E K E L T H S R R G S M S S V T K L S G L F G D T Q S K D P K P E	720
Db	606	MGAVFSGITVYCVCDHRRKDVA V V Q R K E K E L T H S R R G S M S S V T K L S G L F G D T Q S K D P K P E	665
Qy	721	AILTPLMHNGKLATPGNTAKMLIKADQHHLDTALPTPESTPTLQQKRKPSRGSREWERN	780
Db	666	AILTPLMHNGKLATPGNTAKMLIKADQHHLDTALPTPESTPTLQQKREPSRGTREWERN	725
Qy	781	QNLINACTKDMPPMGSPVIPTDLPLRASPSHIPSVVVLPI T Q Q G Y Q H E Y V D Q P K M S E V A Q	840
Db	726	QNLINACTKDMPPMGSPVIPTDLPLRASPSHIPSVVVLPI T Q Q G Y Q H E Y V D Q P K M S E V A Q	785
Qy	841	MALEDQAATLEYKTIKEHLSSKSPNHGVNLVENLDSLPPKVPQREASLGPPGASLSQTGL	900
Db	786	MALEDQAATLEYKTIKEHLSSKSPNHGVNLVENLDSLPPKVPQREASLGPPGASLSQTGL	845
Qy	901	SKRLEMHHSSSYGVDYKRSYPTNSLTRSHQAT	932
Db	846	SKRLEMHHSSSYGVDYKRSYPTNSLTRSHLT	877

RESULT 9

AAB95139

ID AAB95139 standard; protein; 699 AA.

XX

AC AAB95139;

XX

DT 26-JUN-2001 (first entry)

XX

DE Human protein sequence SEQ ID NO:17154.

XX

KW Human; primer; detection; diagnosis; antisense therapy; gene therapy.

XX

OS Homo sapiens.

XX

PN EP1074617-A2.

XX

PD 07-FEB-2001.

XX

PF 28-JUL-2000; 2000EP-00116126.

XX

PR 29-JUL-1999; 99JP-00248036.

PR 27-AUG-1999; 99JP-00300253.

PR 11-JAN-2000; 2000JP-00118776.

PR 02-MAY-2000; 2000JP-00183767.

PR 09-JUN-2000; 2000JP-00241899.

XX

PA (HELI-) HELIX RES INST.

XX

PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;

PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;

XX

DR WPI; 2001-318749/34.

XX

PT Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.

XX

PS Claim 8; SEQ ID NO 17154; 2537pp + Sequence Listing; English.

XX

CC The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: CC (a) an oligo-dT primer and an oligonucleotide complementary to the CC complementary strand of a polynucleotide which comprises one of the 5602 CC nucleotide sequences defined in the specification, where the CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination CC of an oligonucleotide comprising a sequence complementary to the CC complementary strand of a polynucleotide which comprises a 5'-end CC sequence and an oligonucleotide comprising a sequence complementary to a CC polynucleotide which comprises a 3'-end sequence, where the CC oligonucleotide comprises at least 15 nucleotides and the combination of CC the 5'-end sequence/3'-end sequence is selected from those defined in the CC specification. The primer sets can be used in antisense therapy and in CC gene therapy. The primers are useful for synthesising polynucleotides, CC particularly full-length cDNAs. The primers are also useful for the

CC detection and/or diagnosis of the abnormality of the proteins encoded by
CC the full-length cDNAs. The primers allow obtaining of the full-length
CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893
CC represent human amino acid sequences; and AAH13629 to AAH13632 represent
CC oligonucleotides, all of which are used in the exemplification of the
CC present invention

XX

SQ Sequence 699 AA;

Query Match 67.5%; Score 3677; DB 4; Length 699;
Best Local Similarity 100.0%; Pred. No. 1.2e-307;
Matches 699; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      332 MLDIASVFTGRFKEQKSPDSTWTPVDERVPKPRPGCCAGSSSLERYATSNEFPDDTLNF 391
          |||
Db       1 MLDIASVFTGRFKEQKSPDSTWTPVDERVPKPRPGCCAGSSSLERYATSNEFPDDTLNF 60

Qy      392 IKTHPLMDEAVPSIFNRPWFLRTMVRYRLTKIAVDTAAGPYQNHTVFLGSEKGIILKFL 451
          |||
Db       61 IKTHPLMDEAVPSIFNRPWFLRTMVRYRLTKIAVDTAAGPYQNHTVFLGSEKGIILKFL 120

Qy      452 ARIGNSGFLNDSLFLLEMSVYNSEKCSYDGVEDKRIMGMQLDRASSSLYVAFSTCVIKVP 511
          |||
Db      121 ARIGNSGFLNDSLFLLEMSVYNSEKCSYDGVEDKRIMGMQLDRASSSLYVAFSTCVIKVP 180

Qy      512 LGR CERH GKCKKTCIASRDPYCGWIKEGGACSHLSPNSRLTFEQDIERGNTDGLGDCHNS 571
          |||
Db      181 LGR CERH GKCKKTCIASRDPYCGWIKEGGACSHLSPNSRLTFEQDIERGNTDGLGDCHNS 240

Qy      572 FVALNGHSSSLPSTTTSDSTAQEGYESRGGMLDWKHLSDPDSTDPLGAVSSH NHQDKK 631
          |||
Db      241 FVALNGHSSSLPSTTTSDSTAQEGYESRGGMLDWKHLSDPDSTDPLGAVSSH NHQDKK 300

Qy      632 GVIRESYLK GHDQLVPVTL LAIAVILAFVMGAVFSGITVYCVCDHRRKDVAVVQRKEKEL 691
          |||
Db      301 GVIRESYLK GHDQLVPVTL LAIAVILAFVMGAVFSGITVYCVCDHRRKDVAVVQRKEKEL 360

Qy      692 THSR RGSMS SVTKLSGLFGDTQSKDPKPEAILTPLMHNGKLATPGNTAKMLIKADQHHL D 751
          |||
Db      361 THSR RGSMS SVTKLSGLFGDTQSKDPKPEAILTPLMHNGKLATPGNTAKMLIKADQHHL D 420

Qy      752 LTALPTPESTPTLQQKRKPSRGSREWERNQN LINACTKDMPPMGSPVIPTDLPLRASPSH 811
          |||
Db      421 LTALPTPESTPTLQQKRKPSRGSREWERNQN LINACTKDMPPMGSPVIPTDLPLRASPSH 480

Qy      812 IPSVVVLPI TQQGYQHEYVDQPKMSEVAQMALEDQAATLEYKTIKEHLSSKSPNHGVNLV 871
          |||
Db      481 IPSVVVLPI TQQGYQHEYVDQPKMSEVAQMALEDQAATLEYKTIKEHLSSKSPNHGVNLV 540

Qy      872 ENLDSLPPKVPQREASLGPPGASLSQTGLSKRLEMHHSSSYGVDYKRSYPTNSLTRSHQA 931
          |||
Db      541 ENLDSLPPKVPQREASLGPPGASLSQTGLSKRLEMHHSSSYGVDYKRSYPTNSLTRSHQA 600

Qy      932 TTLKRNTN SSNSSHLSRNQS FGRGDNPPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNA 991
          |||
Db      601 TTLKRNTN SSNSSHLSRNQS FGRGDNPPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNA 660
```

QY 992 YNSLTRSGLKRTPSLKPDPVPPKPSFAPLSTSMKPNDACT 1030
|||||
Db 661 YNSLTRSGLKRTPSLKPDPVPPKPSFAPLSTSMKPNDACT 699

RESULT 10

AAB23043

ID AAB23043 standard; protein; 630 AA.

XX

AC AAB23043;

XX

DT 16-JAN-2001 (first entry)

XX

DE Human semaphorin protein-like splice variant, SECX pCR2.1-2864933.

XX

KW SECX protein; human; secreted; membrane-associated; cancer;
KW proliferation regulator; differentiation regulator; non-malignant tumour;
KW immune disorder; autoimmune disease; transplant rejection; allergy; AIDS;
KW infection; inflammatory disorder; arthritis; haematopoietic disorder;
KW skin disorder; cardiovascular disorder; atherosclerosis; restenosis;
KW neurological disease; Alzheimer's disease; trauma; wounding;
KW spinal cord injury; skeletal disorder; cytostatic; immunosuppressive;
KW anti-HIV; antiinflammatory; antiarthritic; antiarteriosclerotic;
KW neuroprotective; vulnerary; antiallergic; antimicrobial; cardiant;
KW dermatological; gene therapy.

XX

OS Homo sapiens.

XX

PN WO200053742-A2.

XX

PD 14-SEP-2000.

XX

PF 09-MAR-2000; 2000WO-US006280.

XX

PR 09-MAR-1999; 99US-0123667P.

PR 08-MAR-2000; 2000US-0520781P.

XX

PA (CURA-) CURAGEN CORP.

XX

PI Shimkets RA;

XX

DR WPI; 2000-594318/56.

DR N-PSDB; AAA93630.

XX

PT Novel human membrane associated or secreted polypeptides and
PT polynucleotides useful for diagnosis, prevention and treatment of
PT pathological states such as cancer, immune, cardiovascular and
PT neurological disorders.

XX

PS Claim 1; Fig 15; 151pp; English.

XX

CC Sequences AAB23029-B23048 represent human SECX proteins. The SECX
CC proteins of the invention are either secreted or membrane-associated
CC proteins and act as regulator of cellular proliferation and
CC differentiation. SECX proteins or nucleotides are useful for diagnosing
CC the presence of, or predisposition to, a disease associated with altered

CC levels of SECX proteins and nucleotides. The SECX proteins are also
 CC useful to screen compounds that modulate SECX activity or expression. The
 CC interaction of a SECX protein with other cellular proteins may be useful
 CC to modulate the activity of a partner protein, cellular proliferation,
 CC cellular differentiation and cell survival. SECX nucleotides are useful
 CC for the recombinant expression of SECX protein, and may be used detect
 CC SECX mRNA or genetic lesions in the SECX gene. They may also be used to
 CC modulate SECX expression (e.g., using antisense oligonucleotides). SECX
 CC nucleic acid sequences are also useful for identifying a cell or tissue
 CC type in a biological sample, and in forensic biology. SECX primers or
 CC probes are useful for detecting the presence of SECX nucleotides and for
 CC screening tissue cultures for contamination. Diseases that may be treated
 CC or prevented using SECX proteins or nucleotides include cancer (e.g.,
 CC colorectal carcinoma, prostate cancer), benign tumours, immune disorders
 CC (including autoimmune diseases, transplant rejection, allergies, AIDS),
 CC infections, inflammatory disorders, arthritis, haematopoietic disorders,
 CC skin disorders, cardiovascular disorders, atherosclerosis, restenosis,
 CC neurological diseases (e.g., Alzheimer's disease), trauma (e.g., surgical
 CC or traumatic wounds, spinal cord injury), and skeletal disorders
 XX
 SQ Sequence 630 AA;

Query Match 61.9%; Score 3373; DB 3; Length 630;
 Best Local Similarity 99.8%; Pred. No. 1.8e-281;
 Matches 628; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy	17	GAGFPEDSEPI	SISHGNYTKQYPVFVGHK	PGRNTTQRHRLDIQMIMIMNGTLYIAARDHI	76
		:			
Db	1	GSGFPEDSEPI	SISHGNYTKQYPVFVGHK	PGRNTTQRHRLDIQMIMIMNGTLYIAARDHI	60
Qy	77	YTVDIDTSHTEEIYCSK	KLTKWSRQADVDTCRMKGKHKDECHNFIK	VLLKKNDDALFVCG	136
Db	61	YTVDIDTSHTEEIYCSK	KLTKWSRQADVDTCRMKGKHKDECHNFIK	VLLKKNDDALFVCG	120
Qy	137	TNAFNPSCRNYKMDTLE	PFSGDEFSGMARCPYDAKHANVALFADGKLYSATVTDFLAIDAV	196	
Db	121	TNAFNPSCRNYKMDTLE	PFSGDEFSGMARCPYDAKHANVALFADGKLYSATVTDFLAIDAV	180	
Qy	197	IYRSLGESPTLRTVKH	DSKWLKEPYFVQAVDYGDIYFFFREIAVEYNTMGKVVFPRAQ	256	
Db	181	IYRSLGESPTLRTVKH	DSKWLKEPYFVQAVDYGDIYFFFREIAVEYNTMGKVVFPRAQ	240	
Qy	257	VCKNDMGGSQRVLEKQ	WTSFLKARLNCSVPGDSHFYFNILQAVTDVIRINGRDVVLATFS	316	
Db	241	VCKNDMGGSQRVLEKQ	WTSFLKARLNCSVPGDSHFYFNILQAVTDVIRINGRDVVLATFS	300	
Qy	317	TPYNSIPGSAVCAYDML	DIASVFTGRFKEQKSPDSTWTFVPDERVPKPRPGCCAGSSSLE	376	
Db	301	TPYNSIPGSAVCAYDML	DIASVFTGRFKEQKSPDSTWTFVPDERVPKPRPGCCAGSSSLE	360	
Qy	377	RYATSNEFPDDTLNFI	KTHPLMDEAVPSIFNRPWFRLTMVRYRLTKIAVDTAAGPYQNHT	436	
Db	361	RYATSNEFPDDTLNFI	KTHPLMDEAVPSIFNRPWFRLTMVRYRLTKIAVDTAAGPYQNHT	420	
Qy	437	VVFLGSEKGIILKFLA	RIGNSGFLNDSLFLLEEMSVYNSEKCSYDGVEDKRIMGMQLDRAS	496	
Db	421	VVFLGSEKGIILKFLA	RIGNSGFLNDSLFLLEEMSVYNSEKCSYDGVEDKRIMGMQLDRAS	480	

Qy 497 SSLYVAFSTCVIKVPLGRCERHGKCKKTCIASRDPYCGWKEGGACSHLSPNSRLTFEQD 556
 |||
 Db 481 SSLYVAFSTCVIKVPLGRCERHGKCKKTCIASRDPYCGWKEGGACSHLSPNSRLTFEQD 540
 Qy 557 IERGNTDGLGDCHNSFVALNGHSSSLLPSTTTSDSTAQEGYESRGGMLDWKHLSDPDST 616
 |||
 Db 541 IERGNTDGLGDCHNSFVALNGHSSSLLPSTTTSDSTAQEGYESRGGMLDWKHLSDPDST 600
 Qy 617 DPLGAVSSHNHQDKKGVIRESYLKGHQDL 645
 |||
 Db 601 DPLGAVSSHNHQDKKGVIRESYLKGHQDL 629

RESULT 11

ADA23307

ID ADA23307 standard; protein; 630 AA.

XX

AC ADA23307;

XX

DT 20-NOV-2003 (first entry)

XX

DE Human SECX polypeptide.

XX

KW Human; secreted polypeptide; membrane-associated polypeptide; SECX; SEC1;

KW SEC2; SEC3; SEC4; SEC5; SEC6; SEC7; SEC8; SEC9; SEC10; SEC11; SEC12;

KW SEC13; SEC14; SEC15; SECX-associated disorder; lung cancer;

KW cardiovascular disease; oncology disease; immune disorder;

KW autoimmune disease; transplant rejection; allergy; AIDS; infections;

KW inflammatory disorder; arthritis; haematopoietic disorder; skin disorder;

KW atherosclerosis; restenosis; neurological disease; Alzheimer's disease;

KW trauma; wounds; spinal cord injury; skeletal disorder; cytostatic;

KW antiinflammatory; immunosuppressive; anti-HIV; antiarthritic;

KW antiarteriosclerotic; cardiant; neuroprotective; nootropic; vulnerary;

KW antiallergic; cardiant; dermatological.

XX

OS Homo sapiens.

XX

PN US2003054514-A1.

XX

PD 20-MAR-2003.

XX

PF 19-SEP-2001; 2001US-00957187.

XX

PR 09-MAR-1999; 99US-0123667P.

PR 04-JAN-2000; 2000US-0174485P.

PR 08-MAR-2000; 2000US-00520781.

PR 19-SEP-2000; 2000US-0233798P.

PR 20-SEP-2000; 2000US-0234082P.

XX

PA (SHIM/) SHIMKETS R A.

PA (LARO/) LAROCHELLE W J.

XX

PI Shimkets RA, Larochelle WJ;

XX

DR WPI; 2003-540616/51.

DR N-PSDB; ADA23306.

Qy 497 SSLYVAFSTCVIKVPLGRGERHGKCKKTCIASRDPYCGWIKEGGACSHLSPNSRLTFEQD 556
 |||
 Db 481 SSLYVAFSTCVIKVPLGRGERHGKCKKTCIASRDPYCGWIKEGGACSHLSPNSRLTFEQD 540
 Qy 557 IERGNTDGLGDCHNSFVALNGHSSSLPSTTTSDSTAQEGYESRGGMLDWKHLDSPDST 616
 |||
 Db 541 IERGNTDGLGDCHNSFVALNGHSSSLPSTTTSDSTAQEGYESRGGMLDWKHLDSPDST 600
 Qy 617 DPLGAVSSHNHQDKKGVIRESYLKGHQDL 645
 |||
 Db 601 DPLGAVSSHNHQDKKGVIRESYLKGHQDL 629

RESULT 12

ADA23360

ID ADA23360 standard; protein; 626 AA.

XX

AC ADA23360;

XX

DT 20-NOV-2003 (first entry)

XX

DE Human SECX polypeptide, SEC3 #2.

XX

KW Human; secreted polypeptide; membrane-associated polypeptide; SECX; SEC1;

KW SEC2; SEC3; SEC4; SEC5; SEC6; SEC7; SEC8; SEC9; SEC10; SEC11; SEC12;

KW SEC13; SEC14; SEC15; SECX-associated disorder; lung cancer;

KW cardiovascular disease; oncology disease; immune disorder;

KW autoimmune disease; transplant rejection; allergy; AIDS; infections;

KW inflammatory disorder; arthritis; haematopoietic disorder; skin disorder;

KW atherosclerosis; restenosis; neurological disease; Alzheimer's disease;

KW trauma; wounds; spinal cord injury; skeletal disorder; cytostatic;

KW antiinflammatory; immunosuppressive; anti-HIV; antiarthritic;

KW antiarteriosclerotic; cardiant; neuroprotective; nootropic; vulnerary;

KW antiallergic; cardiant; dermatological.

XX

OS Homo sapiens.

XX

PN US2003054514-A1.

XX

PD 20-MAR-2003.

XX

PF 19-SEP-2001; 2001US-00957187.

XX

PR 09-MAR-1999; 99US-0123667P.

PR 04-JAN-2000; 2000US-0174485P.

PR 08-MAR-2000; 2000US-00520781.

PR 19-SEP-2000; 2000US-0233798P.

PR 20-SEP-2000; 2000US-0234082P.

XX

PA (SHIM/) SHIMKETS R A.

PA (LARO/) LAROCHELLE W J.

XX

PI Shimkets RA, Larochelle WJ;

XX

DR WPI; 2003-540616/51.

DR N-PSDB; ADA23359.

XX
PT New SECX nucleic acids, useful for treating or diagnosing a disorder
PT e.g., lung cancer, cardiovascular and oncology diseases, immune disorder,
PT and autoimmune disease.
XX
PS Claim 12; Page 7; 118pp; English.
XX
CC The present invention relates to the isolation of human secreted or
CC membrane-associated (SECX) polypeptides designated SEC1-SEC15, and the
CC polynucleotide sequences encoding them. Also disclosed is a method for
CC screening for a modulator of activity or latency of SECX. The SECX
CC polypeptide and polynucleotide sequences may be used for treating or
CC preventing SECX-associated disorders such as lung cancer, cardiovascular
CC and oncology diseases, immune disorders, autoimmune diseases, transplant
CC rejection, allergy, AIDS, infections, inflammatory disorders, arthritis,
CC haematopoietic disorders, skin disorders, atherosclerosis, restenosis,
CC neurological diseases (e.g. Alzheimer's disease), trauma, wounds, spinal
CC cord injuries, and skeletal disorders. The present sequence represents a
CC SECX polypeptide of the invention.
XX
SQ Sequence 626 AA;

Query Match 61.7%; Score 3362; DB 6; Length 626;
Best Local Similarity 100.0%; Pred. No. 1.6e-280;
Matches 626; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	19	GFPEDSEPI	SHGNYTKQYPVFVGHKPG	RNTTQRHRLDIQMIMIMNGTLYIAARDHIYT	78
Db	1	GFPEDSEPI	SHGNYTKQYPVFVGHKPG	RNTTQRHRLDIQMIMIMNGTLYIAARDHIYT	60
Qy	79	VDIDTSHTEEIYCSK	KLTKWSRQADVDTCRMKGKHKDECHNFIKVL	LKKND DALFVCGTN	138
Db	61	VDIDTSHTEEIYCSK	KLTKWSRQADVDTCRMKGKHKDECHNFIKVL	LKKND DALFVCGTN	120
Qy	139	AFNPSCRNYKMDTLE	PFSGDEFSGMARCPYDAKHANVALFADGKLYS	ATVTDFLAIDAVIY	198
Db	121	AFNPSCRNYKMDTLE	PFSGDEFSGMARCPYDAKHANVALFADGKLYS	ATVTDFLAIDAVIY	180
Qy	199	RSLGESPTLRTVKH	DSKWLKEPYFVQAVDYGDIYFFFREIAVEYN	TMGKVVFPRAQVC	258
Db	181	RSLGESPTLRTVKH	DSKWLKEPYFVQAVDYGDIYFFFREIAVEYN	TMGKVVFPRAQVC	240
Qy	259	KNDMGGSQRVLEKQ	WTSFLKARLNCSVPGDSHFYFNILQAVTDVIRINGR	DRVVLATFSTP	318
Db	241	KNDMGGSQRVLEKQ	WTSFLKARLNCSVPGDSHFYFNILQAVTDVIRINGR	DRVVLATFSTP	300
Qy	319	YNSIPGSAVCAYDML	DIASVFTGRFKEQKSPDSTWTPVPDERVPKPRPGCCAGSSSLERY	378	
Db	301	YNSIPGSAVCAYDML	DIASVFTGRFKEQKSPDSTWTPVPDERVPKPRPGCCAGSSSLERY	360	
Qy	379	ATSNEFPDDTLNFI	KTHPLMDEAVPSIFNRPWFLRTMVRYRLTKIAVDTAAGPYQNHTVV	438	
Db	361	ATSNEFPDDTLNFI	KTHPLMDEAVPSIFNRPWFLRTMVRYRLTKIAVDTAAGPYQNHTVV	420	
Qy	439	FLGSEKGIILKFLAR	IGNSGFLNDSLFLLEEMSVYNSEKCSYDGVEDKRIMGMQLDRASSS	498	
Db	421	FLGSEKGIILKFLAR	IGNSGFLNDSLFLLEEMSVYNSEKCSYDGVEDKRIMGMQLDRASSS	480	

Qy 499 LYVAFSTCVIKVPLGRCERHGKCKKTCIASRDPYCGWKEGGACSHLSPNSRLTFEQDIE 558
 |||
 Db 481 LYVAFSTCVIKVPLGRCERHGKCKKTCIASRDPYCGWKEGGACSHLSPNSRLTFEQDIE 540
 Qy 559 RGNTDGLGDCHNSFVALNGHSSSLLPSTTTSDSTAQEGYESRGGMLDWKHLLDSPDSTDP 618
 |||
 Db 541 RGNTDGLGDCHNSFVALNGHSSSLLPSTTTSDSTAQEGYESRGGMLDWKHLLDSPDSTDP 600
 Qy 619 LGAVSSHNHQDKKGVIRESYLKGHQDQ 644
 |||
 Db 601 LGAVSSHNHQDKKGVIRESYLKGHQDQ 626

RESULT 13

AAB95317

ID AAB95317 standard; protein; 574 AA.

XX

AC AAB95317;

XX

DT 26-JUN-2001 (first entry)

XX

DE Human protein sequence SEQ ID NO:17568.

XX

KW Human; primer; detection; diagnosis; antisense therapy; gene therapy.

XX

OS Homo sapiens.

XX

PN EP1074617-A2.

XX

PD 07-FEB-2001.

XX

PF 28-JUL-2000; 2000EP-00116126.

XX

PR 29-JUL-1999; 99JP-00248036.

PR 27-AUG-1999; 99JP-00300253.

PR 11-JAN-2000; 2000JP-00118776.

PR 02-MAY-2000; 2000JP-00183767.

PR 09-JUN-2000; 2000JP-00241899.

XX

PA (HELI-) HELIX RES INST.

XX

PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;

PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;

XX

DR WPI; 2001-318749/34.

XX

PT Primer sets for synthesizing polynucleotides, particularly the 5602 full-
 PT length cDNAs defined in the specification, and for the detection and/or
 PT diagnosis of the abnormality of the proteins encoded by the full-length
 PT cDNAs.

XX

PS Claim 8; SEQ ID NO 17568; 2537pp + Sequence Listing; English.

XX

CC The present invention describes primer sets for synthesising 5602 full-
 CC length cDNAs defined in the specification. Where a primer set comprises:
 CC (a) an oligo-dT primer and an oligonucleotide complementary to the

CC complementary strand of a polynucleotide which comprises one of the 5602
 CC nucleotide sequences defined in the specification, where the
 CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
 CC of an oligonucleotide comprising a sequence complementary to the
 CC complementary strand of a polynucleotide which comprises a 5'-end
 CC sequence and an oligonucleotide comprising a sequence complementary to a
 CC polynucleotide which comprises a 3'-end sequence, where the
 CC oligonucleotide comprises at least 15 nucleotides and the combination of
 CC the 5'-end sequence/3'-end sequence is selected from those defined in the
 CC specification. The primer sets can be used in antisense therapy and in
 CC gene therapy. The primers are useful for synthesising polynucleotides,
 CC particularly full-length cDNAs. The primers are also useful for the
 CC detection and/or diagnosis of the abnormality of the proteins encoded by
 CC the full-length cDNAs. The primers allow obtaining of the full-length
 CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
 CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893
 CC represent human amino acid sequences; and AAH13629 to AAH13632 represent
 CC oligonucleotides, all of which are used in the exemplification of the
 CC present invention
 XX
 SQ Sequence 574 AA;

Query Match 54.7%; Score 2980.5; DB 4; Length 574;
 Best Local Similarity 90.7%; Pred. No. 1.2e-247;
 Matches 574; Conservative 0; Mismatches 0; Indels 59; Gaps 1;

Qy 398 MDEAVPSIFNRPWFLRTMVRRLTKIAVDTAAGPYQNHTVVFLGSEKGIILKFLARIGNS 457
 ||||||||||||||||
 Db 1 MDEAVPSIFNRPWFLRTMVR----- 20

Qy 458 GFLNDSLFLLEEMSVYNSEKCSYDGVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGR CER 517
 ||||||||||||||||||||||||||||||||||||||||
 Db 21 -----CSYDGVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGR CER 61

Qy 518 HGKCKKTCIASRDPYCGWIKEGGACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALNG 577
 ||||||||||||||||||||||||||||||||||||||||
 Db 62 HGKCKKTCIASRDPYCGWIKEGGACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALNG 121

Qy 578 HSSSLLPSTTTSDSTAQEGYESRGGMLDWKHL L DSPDST DPLGAVSSH NHQDKKGVIRE S 637
 ||||||||||||||||||||||||||||||||||||||||
 Db 122 HSSSLLPSTTTSDSTAQEGYESRGGMLDWKHL L DSPDST DPLGAVSSH NHQDKKGVIRE S 181

Qy 638 YLK GHDQLVPV TLLAIAVILAFVMGAVFSGITVYCVCDHRRKDVA VVQRKEKELTHSRRG 697
 ||||||||||||||||||||||||||||||||||||||||
 Db 182 YLK GHDQLVPV TLLAIAVILAFVMGAVFSGITVYCVCDHRRKDVA VVQRKEKELTHSRRG 241

Qy 698 SMSSVTKL SGLFGDTQSKDPKPEAILT PLMHNGKLATPGNTAKMLIKADQHHLDTALPT 757
 ||||||||||||||||||||||||||||||||||||||||
 Db 242 SMSSVTKL SGLFGDTQSKDPKPEAILT PLMHNGKLATPGNTAKMLIKADQHHLDTALPT 301

Qy 758 PESTPTLQQKRKPSRGSREWER NQN LINACTKDMPPMGSPVIPTDLPLRASPSHIP SVVV 817
 ||||||||||||||||||||||||||||||||||||||||
 Db 302 PESTPTLQQKRKPSRGSREWER NQN LINACTKDMPPMGSPVIPTDLPLRASPSHIP SVVV 361

Qy 818 LPITQQGYQHEYVDQPKMSEVAQMALEDQAATLEYKTIKEHLSSKSPNHGVNLVENLDSL 877
 ||||||||||||||||||||||||||||||||||||||||
 Db 362 LPITQQGYQHEYVDQPKMSEVAQMALEDQAATLEYKTIKEHLSSKSPNHGVNLVENLDSL 421

Qy 878 PPKVPQREASLGPPGASLSQTGLSKRLEMHHSSSYGVDYKRSYPTNSLTRSHQATTLKRN 937
 |||
 Db 422 PPKVPQREASLGPPGASLSQTGLSKRLEMHHSSSYGVDYKRSYPTNSLTRSHQATTLKRN 481
 Qy 938 NTNSSNSSHLNRNQSFRGDNPPPPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTR 997
 |||
 Db 482 NTNSSNSSHLNRNQSFRGDNPPPPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTR 541
 Qy 998 SGLKRTPSLKPDPVPPKPSFAPLSTSMKPNDACT 1030
 |||
 Db 542 SGLKRTPSLKPDPVPPKPSFAPLSTSMKPNDACT 574

RESULT 14

AAB94104

ID AAB94104 standard; protein; 562 AA.

XX

AC AAB94104;

XX

DT 26-JUN-2001 (first entry)

XX

DE Human protein sequence SEQ ID NO:14328.

XX

KW Human; primer; detection; diagnosis; antisense therapy; gene therapy.

XX

OS Homo sapiens.

XX

PN EP1074617-A2.

XX

PD 07-FEB-2001.

XX

PF 28-JUL-2000; 2000EP-00116126.

XX

PR 29-JUL-1999; 99JP-00248036.

PR 27-AUG-1999; 99JP-00300253.

PR 11-JAN-2000; 2000JP-00118776.

PR 02-MAY-2000; 2000JP-00183767.

PR 09-JUN-2000; 2000JP-00241899.

XX

PA (HELI-) HELIX RES INST.

XX

PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;

PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;

XX

DR WPI; 2001-318749/34.

XX

PT Primer sets for synthesizing polynucleotides, particularly the 5602 full-
 PT length cDNAs defined in the specification, and for the detection and/or
 PT diagnosis of the abnormality of the proteins encoded by the full-length
 PT cDNAs.

XX

PS Claim 8; SEQ ID NO 14328; 2537pp + Sequence Listing; English.

XX

CC The present invention describes primer sets for synthesising 5602 full-
 CC length cDNAs defined in the specification. Where a primer set comprises:
 CC (a) an oligo-dT primer and an oligonucleotide complementary to the

CC complementary strand of a polynucleotide which comprises one of the 5602
 CC nucleotide sequences defined in the specification, where the
 CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
 CC of an oligonucleotide comprising a sequence complementary to the
 CC complementary strand of a polynucleotide which comprises a 5'-end
 CC sequence and an oligonucleotide comprising a sequence complementary to a
 CC polynucleotide which comprises a 3'-end sequence, where the
 CC oligonucleotide comprises at least 15 nucleotides and the combination of
 CC the 5'-end sequence/3'-end sequence is selected from those defined in the
 CC specification. The primer sets can be used in antisense therapy and in
 CC gene therapy. The primers are useful for synthesising polynucleotides,
 CC particularly full-length cDNAs. The primers are also useful for the
 CC detection and/or diagnosis of the abnormality of the proteins encoded by
 CC the full-length cDNAs. The primers allow obtaining of the full-length
 CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
 CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893
 CC represent human amino acid sequences; and AAH13629 to AAH13632 represent
 CC oligonucleotides, all of which are used in the exemplification of the
 CC present invention
 XX
 SQ Sequence 562 AA;

Query Match 54.2%; Score 2952; DB 4; Length 562;
 Best Local Similarity 100.0%; Pred. No. 3.2e-245;
 Matches 562; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	469	MSVYNSEKCSYDGVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRCERHGKCKKTCIAS	528
Db	1	MSVYNSEKCSYDGVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRCERHGKCKKTCIAS	60
Qy	529	RDPYCGWIKEGGACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALNGHSSSLPSTTT	588
Db	61	RDPYCGWIKEGGACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALNGHSSSLPSTTT	120
Qy	589	SDSTAQEGYESRGGMLDWKHLSDPDSTDPLGAVSSHNHQDKKGVIRESYLKGHDLQVLPV	648
Db	121	SDSTAQEGYESRGGMLDWKHLSDPDSTDPLGAVSSHNHQDKKGVIRESYLKGHDLQVLPV	180
Qy	649	TLIAIAVILAFVMGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRGSMSSVTKL SGL	708
Db	181	TLIAIAVILAFVMGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRGSMSSVTKL SGL	240
Qy	709	FGDTQSKDPKPEAILTPLMHNGKLATPGNTAKMLIKADQHHLDTALPTPESTPTLQQKR	768
Db	241	FGDTQSKDPKPEAILTPLMHNGKLATPGNTAKMLIKADQHHLDTALPTPESTPTLQQKR	300
Qy	769	KPSRGSREWERNQNLINACTKDMPPMGSPVIPTDLPLRASPSHIPSVVVLPI TQQGYQHE	828
Db	301	KPSRGSREWERNQNLINACTKDMPPMGSPVIPTDLPLRASPSHIPSVVVLPI TQQGYQHE	360
Qy	829	YVDQPKMSEVAQMALEDQAATLEYKTIKEHLSSKSPNHGVNLVENLDSLPPKVPQREASL	888
Db	361	YVDQPKMSEVAQMALEDQAATLEYKTIKEHLSSKSPNHGVNLVENLDSLPPKVPQREASL	420
Qy	889	GPPGASLSQTGLSKRLEMHHSSSYGV DYKRSYPTNSLTRSHQATTLKRNNNTSSNSSHLS	948
Db	421	GPPGASLSQTGLSKRLEMHHSSSYGV DYKRSYPTNSLTRSHQATTLKRNNNTSSNSSHLS	480

Qy 949 RNQSFGRGDNPPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRTPSLKP 1008
 |||
 Db 481 RNQSFGRGDNPPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRTPSLKP 540
 Qy 1009 DVPPKPSFAPLSTSMKPNDACT 1030
 |||
 Db 541 DVPPKPSFAPLSTSMKPNDACT 562

RESULT 15

AAM93444

ID AAM93444 standard; protein; 562 AA.

XX

AC AAM93444;

XX

DT 06-NOV-2001 (first entry)

XX

DE Human polypeptide, SEQ ID NO: 3088.

XX

KW Human; full length cDNA; cDNA synthesis; oligo-capping.

XX

OS Homo sapiens.

XX

PN EP1130094-A2.

XX

PD 05-SEP-2001.

XX

PF 07-JUL-2000; 2000EP-00114089.

XX

PR 08-JUL-1999; 99JP-00194486.

PR 11-JAN-2000; 2000JP-00118774.

PR 02-MAY-2000; 2000JP-00183765.

XX

PA (HELI-) HELIX RES INST.

XX

PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;

PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;

XX

DR WPI; 2001-524255/58.

DR N-PSDB; AAK94365.

XX

PT 830 Primers useful for synthesizing full length cDNA clones and their use
 PT in genetic manipulation.

XX

PS Claim 8; SEQ ID NO 3088; 1380pp + Sequence Listing; English.

XX

CC The invention relates to primers for synthesising full length cDNA
 CC clones. 830 cDNA molecules encoding a human protein have been isolated
 CC and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have
 CC been determined. Primers for synthesising the full length cDNA are useful
 CC for clarifying the function of the protein encoded by the cDNA. The full
 CC length clones were obtained by construction of full length enriched cDNA
 CC libraries that were synthesised by the oligo-capping method. The primers
 CC enable the production of the full length cDNA easily without any special
 CC methods. The present sequence is a polypeptide encoded by a full length
 CC human cDNA of the invention. Note: The sequence data for this patent did

CC not form part of the printed specification, but was obtained in CD-ROM
CC format directly from EPO
XX
SQ Sequence 562 AA;

Query Match 54.1%; Score 2947; DB 4; Length 562;
Best Local Similarity 99.8%; Pred. No. 8.7e-245;
Matches 561; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy      469 MSVYNSEKCSYDGVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRRCERHGKCKKTCIAS 528
          |||
Db       1 MSVYNSEKCSYDGVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRRCERHGKCKKTCIAS 60

Qy      529 RDPYCGWIKEGGACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALNGHSSSLPSTTT 588
          |||
Db       61 RDPYCGWIKEGGACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALNGHSSSLPSTTT 120

Qy      589 SDSTAQEGYESRGGMLDWKHLLDSPDSTDPLGAVSSHNHQDKKGVIRESYLKGHDLQVPV 648
          |||
Db      121 SDSTAQEGYESRGGMLDWKHLLDSPDSTDPLGAVSSHNHQDKKGVIRESYLKGHDLQVPV 180

Qy      649 TLLAIAVILAFVMGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRGSMSSVTKLSGL 708
          |||
Db      181 TLLAIAVILAFVMGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRGSMSSVTKLSGL 240

Qy      709 FGDTQSKDPKPEAILTPLMHNGKLATPGNTAKMLIKADQHHLDTALPTPESTPTLQQR 768
          |||
Db      241 FGDTQSKDPKPEAILTPLMHNGKLATPGNTAKMLIKADQHHLDTALPTPESTPTLQQR 300

Qy      769 KPSRGSREWERNQNLINACTKDMPPMGSPVIPTDLPLRASPSHIPSVVVLPIITQQGYQHE 828
          |||
Db      301 KPSRGSREWERNQNLINACTKDMPPMGSPVIPTDLPLRASPSHIPSVVVLPIITQQGYQHE 360

Qy      829 YVDQPKMSEVAQMALEDQAATLEYKTIKEHLSSKSPNHGVNLVENLDSLPPKVPQREASL 888
          |||
Db      361 YVDQPKMSEVAQMALEDQAATLEYKTIKEHLSSKSPNHGVNLVENLDSLPPKVPQREASL 420

Qy      889 GPPGASLSQTGLSKRLEMHHSSSYGVYDKRSYPTNSLTRSHQATTLKRNTNSSNSSHLS 948
          |||
Db      421 GPPGASLSQTGLSKRLEMHHSSSYGVYDKRSYPTNSLTRSHQATTLKRNTNSSNSSHLS 480

Qy      949 RNQSFGRGDNPPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRTPSLKP 1008
          |||
Db      481 RNQSFGRGDSPPPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRTPSLKP 540

Qy     1009 DVPPKPSFAPLSTSMKPNDACT 1030
          |||
Db      541 DVPPKPSFAPLSTSMKPNDACT 562
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Search completed: March 24, 2004, 13:14:21
Job time : 104.009 secs

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OM protein - protein search, using sw model

Run on: March 24, 2004, 13:12:28 ; Search time 32.7132 Seconds
(without alignments)
1625.481 Million cell updates/sec

Title: US-09-856-681A-2
Perfect score: 5450
Sequence: 1 MRSEALLLYFTLLHFAGAGF.....PPKPSFAPLSTSMKPNDACT 1030

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		%					
		Query					
Result		Match	Length	DB	ID		
No.	Score					Description	
1	2361.5	43.3	1086	4	US-09-653-274-4	Sequence 4, Appli	
2	2354	43.2	1070	4	US-09-653-274-8	Sequence 8, Appli	
3	2013.5	36.9	888	4	US-09-077-940A-4	Sequence 4, Appli	
4	1997	36.6	887	4	US-09-077-940A-2	Sequence 2, Appli	
5	1923	35.3	641	4	US-09-653-274-13	Sequence 13, Appl	
6	1519.5	27.9	930	4	US-09-254-594-6	Sequence 6, Appli	
7	1428.5	26.2	929	4	US-09-254-594-3	Sequence 3, Appli	
8	1377.5	25.3	536	4	US-09-653-274-10	Sequence 10, Appl	
9	969.5	17.8	730	1	US-08-121-713D-58	Sequence 58, Appl	
10	969.5	17.8	730	1	US-08-835-268-58	Sequence 58, Appl	
11	969.5	17.8	730	2	US-09-060-692-58	Sequence 58, Appl	

12	969.5	17.8	730	3	US-08-833-391-58	Sequence 58, Appl
13	969.5	17.8	730	4	US-09-060-610-58	Sequence 58, Appl
14	969.5	17.8	730	5	PCT-US94-10151A-58	Sequence 58, Appl
15	880	16.1	650	1	US-08-121-713D-60	Sequence 60, Appl
16	880	16.1	650	1	US-08-835-268-60	Sequence 60, Appl
17	880	16.1	650	2	US-09-060-692-60	Sequence 60, Appl
18	880	16.1	650	3	US-08-833-391-60	Sequence 60, Appl
19	880	16.1	650	4	US-09-060-610-60	Sequence 60, Appl
20	880	16.1	650	5	PCT-US94-10151A-60	Sequence 60, Appl
21	852.5	15.6	655	4	US-08-556-422A-3	Sequence 3, Appli
22	852.5	15.6	771	1	US-08-121-713D-54	Sequence 54, Appl
23	852.5	15.6	771	1	US-08-835-268-54	Sequence 54, Appl
24	852.5	15.6	771	2	US-09-060-692-54	Sequence 54, Appl
25	852.5	15.6	771	3	US-08-833-391-54	Sequence 54, Appl
26	852.5	15.6	771	4	US-09-060-610-54	Sequence 54, Appl
27	852.5	15.6	771	5	PCT-US94-10151A-54	Sequence 54, Appl
28	845	15.5	712	1	US-08-121-713D-64	Sequence 64, Appl
29	845	15.5	712	1	US-08-835-268-64	Sequence 64, Appl
30	845	15.5	712	2	US-09-060-692-64	Sequence 64, Appl
31	845	15.5	712	3	US-08-833-391-64	Sequence 64, Appl
32	845	15.5	712	4	US-09-060-610-64	Sequence 64, Appl
33	845	15.5	712	5	PCT-US94-10151A-64	Sequence 64, Appl
34	779.5	14.3	724	1	US-08-121-713D-62	Sequence 62, Appl
35	779.5	14.3	724	1	US-08-835-268-62	Sequence 62, Appl
36	779.5	14.3	724	2	US-09-060-692-62	Sequence 62, Appl
37	779.5	14.3	724	3	US-08-833-391-62	Sequence 62, Appl
38	779.5	14.3	724	4	US-09-060-610-62	Sequence 62, Appl
39	779.5	14.3	724	5	PCT-US94-10151A-62	Sequence 62, Appl
40	748	13.7	775	4	US-09-308-179B-1	Sequence 1, Appli
41	736.5	13.5	862	4	US-08-556-422A-2	Sequence 2, Appli
42	654.5	12.0	607	4	US-08-556-422A-4	Sequence 4, Appli
43	586	10.8	477	1	US-08-136-922-2	Sequence 2, Appli
44	539	9.9	425	4	US-08-556-422A-7	Sequence 7, Appli
45	462	8.5	295	4	US-08-556-422A-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1

US-09-653-274-4

; Sequence 4, Application US/09653274

; Patent No. 6635742

; GENERAL INFORMATION:

; APPLICANT: Boyle, Bryan J

; APPLICANT: Yeung, George Y

; APPLICANT: Arterburn, Matthew C

; APPLICANT: Mize, Nancy K

; APPLICANT: Tang, Y. Tom

; APPLICANT: Liu, Chenghua

; APPLICANT: Drmanac, Radoje T

; TITLE OF INVENTION: Methods and Maaterials Relating to Semaphorin-Like

; TITLE OF INVENTION: Polypeptides and Polynucleotides

; FILE REFERENCE: HYS-23

; CURRENT APPLICATION NUMBER: US/09/653,274

; CURRENT FILING DATE: 2000-08-31

; PRIOR APPLICATION NUMBER: 09/491,404

; ORGANISM: Homo sapiens
US-09-653-274-8

Query Match 43.2%; Score 2354; DB 4; Length 1070;
Best Local Similarity 45.8%; Pred. No. 1.1e-214;
Matches 506; Conservative 159; Mismatches 295; Indels 144; Gaps 29;

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Qy      20 FPEDESEPISSHGNYTKQYPVFVGHKPGRNTTQRHRLDIQMIMIMNGTLYIAARDHIYTV 79
      |||| ||::  :||:|||| | :| | :| |||| |::: : |||| | | :||
Db      7 FPEDEPLNTVDYHYSRQYPVFRG-RPSGNESQ-HRLDFQLMLKIRDTLYIAGRDQVYTV 64

Qy     80 DIDTSHTEEIYCSKKLTWKSQADVDTCRMKGKHKDECHNFIKVLLKKNDALFVCGTNA 139
      :::  | : ||||:|||| | : | ||||| ||||| : ||: : |||||
Db     65 NLNEMPKEVIPNKKLTWRSRQQDRENCAMKGKHKDECHNFIKVFPVRNDEMVFVCGTNA 124

Qy    140 FNPSCRNYKMDTLEPFGDEFSGMARCPYDAKHANVALFADGKLYSATVTDFLAIDAVIYR 199
      ||| || |:: ||| | :| ||:||||:|: | ||||| ||||| |||| | ||||
Db    125 FNPMSCRYRLSTLEYDGEEISGLARCPFDARQTNVALFADGKLYSATVADFLASDAVIYR 184

Qy    200 SLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYFFFREIAVEYNTMGKVVFPRVAQVCK 259
      |:::  |||:|:||||:||||:| :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db    185 SMGDGSALRTIKYDSKWIKEPHFLHAIEYGNVYVFFFREIAVEHNNLGKAVYSRVARICK 244

Qy    260 NDMGGSQRVLEKQWTSFLKARLNCVPGDSHFYFNILQAVTDVIRINGRDVVLATFSTPY 319
      ||||| ||||| ||||| ||||| ||||:|:|:|:|:|:| | : | :|
Db    245 NDMGGSQRVLEKHWTSFLKARLNCVPGDPFFYFDVLSITDIIQINGIPTVVGVTTLQL 304

Qy    320 NSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVPDERVVKPRPGCCAGSSSLERYA 379
      ||||| ||||:| || || |||||:|||| || ||:|:|:|:|:| || ||
Db    305 NSIPGSAVCAFSMDIEKVFKGRFKEQKTPDSVWTAVPEDKVPKPRPGCCAKHGLAEAYK 364

Qy    380 TSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYLRTKIAVDTAAGPYQNHTVVF 439
      || :||:|:|:|:|:| || | : ||| :| ||||| |:| | :|||:|:|:|
Db    365 TSIDFPDETLSFIKSHPLMDSAVPPIADEPWFTKTRVRYRLTAISVDHSAGPYQNYTVIF 424

Qy    440 LGSEKGIILKFLARIGNSGF-LNDSLFLLEMSVYNSEKCSYDGVEDKRIMGMQLDRASSS 498
      :||| |::|| ||:  | | ||||: ||: || ||| : |||::: :|||:  :
Db    425 VGSEAGMVLKVLAK--TSPFSLNDSVLLEEIEAYNHAKCSAENEEDKKVISLQLDKDHHA 482

Qy    499 LYVAFSTCVIKVPLGRRCERHGKCKKTCIASRDPYCGWIKEGGACSHLSPNSRLT----- 552
      |||||:|:|:|:| ||||:| |||:|||||||:|:| : | :| :| |
Db    483 LYVAFSSCIIRIPLSRCERYGCKKSCIASRDPYCGWLSQ-GSCGRVTPGMLLLTEDFFA 541

Qy    553 -----FEQDIERGNTDGLGDCHNSFVALNGHSSSLPSTTTSDSTAQEGYESRGG-- 602
      :||| | ||| ||||| :||:| || | :| ||
Db    542 FHNHSAEGYEQDTEFGNTAHLGDCH-----EILPTSTTPD-----YKIFGGPT 584

Qy    603 -----MLD-WKHLL-----DSP---DSTDPLGAVSSHNNH 627
      :| | : | | | | | :
Db    585 SDMEVSSSSVTTMASIPEITPKVIDTWRPKLTSSRKFFVQDDPNTSDFTDPLSGI----- 639

Qy    628 QDKKGVIRESYLKGHDQLVPVTLIAIVILAFVMGAVFSGITVYCVCD-HRRKDVAVVQR 686
      ||| | :|:| : :| | |||:| :|: ||| | ||: :
Db    640 --PKGVRWEVQSGESNQMVHMNVLITCVFAAFVLGAFIAGVAVYCYRDMFVRKRNKI--H 695

Qy    687 KEKELTHSRRGSMSSVTKLGLFG----DTQSKDPKPEAILTPLMHNGKLATPGNTAKML 742
      | : | | | | ||:| | : | | :| | :| | :|
```

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Db      696 KDAESAQSCTDSSGSFAKLNGLFDSPVKEYQQNIDSPKLYSNLLTSRKELPPNGDTKSMV 755
Qy      743 IKADQHHLDLTALPTPESTPTLQQRKPSRGSREWERNQNLINACTKDMPPMGSPVIPTD 802
      :      :| ||||| || | | : | : : : | | : |
Db      756 MDHRGQPPELAALPTPESTPVLHQKTLQAMKSHSEKAHGH--GASRKETPQFFPSSPPPH 813
Qy      803 LPLRASPSHIPSVVVLPIITQQGYQHEY-----VDQP---KMSEVAQMALED 845
      || | | ||| :|| | : : | | | : |
Db      814 SPL--SHGHIPSAIVLPNATHDYNTSFSNSNAHKAEEKLQNIHPLTKSSSKRDHRRSVD 871
Qy      846 QAATLEYKTIKEHLSSKSPN-----HGVNLVENLDSL---PPKVPQREASLGPP 891
      || : :|| : | | : : : | : |||| |||| |
Db      872 SRNTL--NDLLKHLNDPNSNPKAIMGDIQMAHQNLMLDPMGSMSEVPPKVPNREASLYSP 929
Qy      892 GASLSQTGLSKRLEMHHSSSY---GVDYKRSYPTNSLTRSHQATTLKRNTNTSSNSSHLS 948
      :| : :|| : : : : : | | | | : : : | | | ||
Db      930 PSTLPRNSPTKRVDVPTTPGVPMTSLERQRGYHKNSSQR-HSISAMPK-NLNSPNGVLLS 987
Qy      949 RNQSFGRGD-NPPPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLT-----RSLGK 1001
      | | || | | :|| || | | :| |||| : | | | :|||
Db      988 RQPSMNRGGYMPPTPTGAKVDYIQ-----GTPVSVHLQPSLSRQSSYTSNGTLPRTGLK 1040
Qy      1002 RTPSLKPDVPPKPSFAPLSTSMKP 1025
      ||||| ||||| || | : | : |
Db      1041 RTPSLKPDVPPKPSFVPQTPSVRP 1064

```

RESULT 3

US-09-077-940A-4

; Sequence 4, Application US/09077940A

; Patent No. 6576441

; GENERAL INFORMATION:

; APPLICANT: KIMURA, Toru et al.

; TITLE OF INVENTION: NOVEL SEMAPHORIN 2 AND GENE ENCODING THE SAME

; FILE REFERENCE: 0020-4426P

; CURRENT APPLICATION NUMBER: US/09/077,940A

; CURRENT FILING DATE: 1998-06-05

; NUMBER OF SEQ ID NOS: 20

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 4

; LENGTH: 888

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-077-940A-4

Query Match 36.9%; Score 2013.5; DB 4; Length 888;

Best Local Similarity 45.3%; Pred. No. 2.3e-182;

Matches 424; Conservative 129; Mismatches 241; Indels 141; Gaps 20;

```

Qy      5 ALLLYFTLLHFAGAGFPEDSEPISISHGNYTKQYPVFVGHKPGRNTTQR--HRLDIQMIM 62
      ||| | | | | | | | | | | :| | | | | | | | | | | :| :
Db      12 ALLLLLLLLGGAGHLFPEDPPPLSVAPRDYLNHYPVVFVSGPGRLTPAEGADDLNIQRVL 71
Qy      63 IMNGTLYIAARDHIYTVDIDTSHTEEIYCSKKLTWKSQADVDTCRMKGKHKDECHNFIK 122
      :| ||:| ||:| | : : : | : : ||||:| : : : ||||| : || ||:|
Db      72 RVNRTLFIGDRDNLYRVELEPPTSTELRYQRKLTWRSNPSDINVCRMKGKQEGECRNFKV 131

```

Qy 123 VLLKKND DALFVCGTNAFNPSCRNYKMDTLEPFGDEFSGMARCPYDAKHANVALFADGKL 182
 ||| ::: |||||:|||| | || :||:| || ||||| |||||:| |
 Db 132 VLLLRDESTLFVCGSNAFN PVCANYSIDTLQPVGDNISGMARCPYDPKHANVALFSDGML 191

Qy 183 YSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYFFRFREIAVE 242
 ::||| |||||: ||||| ||||| ||::| ::||| |||||:|
 Db 192 FTATVTDFLAIDAVIYRSLGDRPTLRTVKHDSKWFKEPYFVHAVEWGS HVYFFRFREIAME 251

Qy 243 YNTMGKVVFPRVAQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDSHFYFNILQAVTDV 302
 :| : ||| |||:|||||: ||| ||||| |||||: ||||| |
 Db 252 FNYLEKVVVSRVARVCKNDVGGSPRVLEKQWTSFLKARLNCSVPGDSHFYFNVLQAVTGV 311

Qy 303 IRINGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVPDERVP 362
 : : || |||| |||| ||||| |||||:| :||| |||: |||||:| |||||::| |
 Db 312 VSLGGRPVVLAVFSTPSNSIPGSAVCAFDLTQVAAVFEGRFREQKSPESIWTFVPEDQVP 371

Qy 363 KPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRLTK 422
 :||| ||| :| | : ||| |||: ||||| ||| : || |||: |||: |||
 Db 372 RPRPGCCAAPGM--QYNASSALPDDILNFVKTHPLMDEAVPSLGHPWILRTLMRHQLTR 429

Qy 423 IAVDTAAGPYQNHTVVFLGSEKGIILKFLAR--IGNSGFLNDSL FLEEMSVYNSEKCSYD 480
 :||| |||: | ||||| ||| :||| | || | :||| | :|
 Db 430 VAVDVGAGPWGNQTVVFLGSEAGTVLKFLVRPNASTSGTSGLSVFLEEFETYRPDRGRP 489

Qy 481 GVED--KRIMGMLDRASSSLYAFSTCVIKVPLGR CERHKGCKKTCIASRDPYCGWIKE 538
 | : :||: ::|| || | || ||: ||: ||: ||: || ||| :
 Db 490 GGGETGQRLLSLELDAASGGLLAAPRCVVRVPVARCQQYSGCMKNCIGSQDPYCGWAPD 549

Qy 539 GGACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALNGHSSSLPSTTTSDSTAQEGYE 598
 | : ||| :| |||| :| ||||
 Db 550 -GSCIFLSPGTAAFEQDVSGASTSGLGDC----- 578

Qy 599 SRGMLDWKHL DSDPDST DPLGAVSSH NHQDKKGVIRESYLK GHDQLVPVTL LAIAVILA 658
 | : || | : || || | : ||
 Db 579 -----TGLLRASLSED RAGLVS VNLLVTSSVAA 606

Qy 659 FVMGAVFSGITV-YCVC DHRRKDVAVVQRKEKE--LTHSRRGSMSSVTKLSGLFGDTQSK 715
 ||: ||| || :| : | ||: || :||: || | | : ||: || | : :
 Db 607 FVVGAVVSGFSVGWVFLRERRELA--RRKDKEAILAHGAGEAVLSVSRL----GERRAQ 660

Qy 716 DP-----KPEAILTPLMHNGKLATPGNTAK-MLIKADQHHLDTALPTPEST 761
 | |||| | : ||| || || ||: | || |||| |
 Db 661 GPGGRRGGGGGGAGVPPEALLAPLMQNG-----WAKATLLQGGPHDLDSGLLPTPEQT 713

Qy 762 PTLQQKRKP-----SRGSREWERNQNLINACTKDMPPMGSPVIPTDLP---LRASPSH 811
 | |||| | : ||| : |||| | ||: | || :| :
 Db 714 P-LPQKRLPTPHPHALGPRAWDH-----GHPLL PASASSS LLLLAPAR 757

Qy 812 IPSVVVLPI TQQGYQHEYVDQPKMSEVAQMALEDQAATLEYKTIKEHLSSKSPNHGVNLV 871
 | | | :| : | | : : :| : :
 Db 758 APEQPPAPGEPTPDGRLYAARPGRASHGDFLTPHASPDRRRV-----SAPTGPLDPA 811

Qy 872 ENLDSL P-PKVPQREASL-----GPPGASLSQT 898
 | || | | || || ||: | :|
 Db 812 SAADGLPRPWSPPPTGSLRRPLGPHAPPAATLRRT 846

US-09-077-940A-2

Query Match 36.6%; Score 1997; DB 4; Length 887;
Best Local Similarity 42.7%; Pred. No. 8.7e-181;
Matches 433; Conservative 132; Mismatches 260; Indels 190; Gaps 25;

[illegible]

Qy 535 WKEGGACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALNGHSSSLPSTTTSDSTAQ 594
 | : |:| | | : ||||: :| ||||
 Db 548 WAPD-GSCIFLRPGTSATFEQDVSGASTSGLGDC----- 580

Qy 595 EGYESRGGMLDWKHLLDSPDSTDPLGAVSSHNHQDKKGVIRESYLKGHQDQLVPVTLAIA 654
 |::| | | | | | :
 Db 581 -----TGLLRASLSDDRAGLVSVNLLVTS 604

Qy 655 VILAFVMGAVFSGITV-YCVCDHRRKDVAVVQRKEKE--LTHSRRGSMSSVTKL----- 705
 : |||:|||| | | : | : | | :||:| | | : ||:|
 Db 605 SVAAFVVGAVVSGFVSGVFWFGLRERRELA--RRKDKEAILAHGGSEAVLSVSRLGERRGT 662

Qy 706 --SGLFGDTQSKDPKPEAILTPLMHNGKLATPGNTAKMLIKADQHHLDTALPTPESTPT 763
 | | | | | | | | | | | | | : | | | | | | | |
 Db 663 GTGGRGGAGGGPGGPPEALLAPLMQNGW-----TKAALLHGGPHDLDLGLLPTPEQTP- 715

Qy 764 LQQRKPSR-----GSREWERNQNLINACTK-----DMPPMGSPVIPTD-- 802
 | | | | : | | | : : |::| : | | :||:
 Db 716 LPQKRLPTTHPHAHALGPAWDHSHALLSASASTSLLLLAHTRAPEQPP-----VPTESG 770

Qy 803 -----LPLRASPSHIPSVVVLPIITQQGYQHEYVDQPKMSEVAQMALEDQAATLEYKTIK 856
 | | | : | | | : : | : :
 Db 771 PESRLCAPRSCRASHPGDFPLTP-----HASPDRRRVVSAPTGPLDSSSVG----- 816

Qy 857 EHLSSKSPNHGVNLVENLDSLP-PKVPQREASL-----GPPGASLSQTGLSKRLEMHHS 909
 | | | | | :|| | | | : | : |
 Db 817 -----DDLPGPWSPPATSSLRRPGHPPTAALRRT-----HT 849

Qy 910 SSYGVVDYKRSYPTNSLTRSHQATTLLKRNNTNSSNSSHLSRNQSFGRGD-NPPPPAP 963
 : | : | | | :||:| | | : | | |
 Db 850 FNSG----EARPGGHRPRRHA-----PADSTHL---LPCGTGERTAPPVP 887

RESULT 5

US-09-653-274-13

; Sequence 13, Application US/09653274

; Patent No. 6635742

; GENERAL INFORMATION:

; APPLICANT: Boyle, Bryan J

; APPLICANT: Yeung, George Y

; APPLICANT: Arterburn, Matthew C

; APPLICANT: Mize, Nancy K

; APPLICANT: Tang, Y. Tom

; APPLICANT: Liu, Chenghua

; APPLICANT: Drmanac, Radoje T

; TITLE OF INVENTION: Methods and Maaterials Relating to Semaphorin-Like

; TITLE OF INVENTION: Polypeptides and Polynucleotides

; FILE REFERENCE: HYS-23

; CURRENT APPLICATION NUMBER: US/09/653,274

; CURRENT FILING DATE: 2000-08-31

; PRIOR APPLICATION NUMBER: 09/491,404

; PRIOR FILING DATE: 2000-01-10

; NUMBER OF SEQ ID NOS: 13

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 13

; LENGTH: 641

; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-653-274-13

Query Match 35.3%; Score 1923; DB 4; Length 641;
Best Local Similarity 55.3%; Pred. No. 5.5e-174;
Matches 362; Conservative 101; Mismatches 118; Indels 74; Gaps 12;

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Qy      20  FPEDESEPISSHGNYTKQYPVFVGHKPGRNTTQRHRLDIQMIMMNGTLYIAARDHIYTV 79
      ||| ||:: :||:|||| | :| | :| ||| |::: : |||| || :||
Db      7  FPEDEDEPLNTVDYHYSRQYPVFRG-RPSGNESQ-HRLDFQLMLKIRDTLYIAGRDQVYTV 64

Qy     80  DIDTSHTEEIYCSKKLTWKSQRQADVDTCRMKGKHKDECHNFIKVLLKKNDDALFVCGTNA 139
      ::: | : ||||:|||| | : | ||||| ||||| : ||: |||||
Db     65  NLNEMPKTEVIPNKKLTWRSRQQDRENCAMKGKHKDECHNFIKVFPVPRNDEMVFVCGTNA 124

Qy    140  FNPSCRNYKMDTLEPFGDEFSGMARCPYDAKHANVALFADGKLYSATVTDFLAIDAVIYR 199
      ||| || |:: || | :| ||:||||:|: | ||||| ||||| ||| |||||
Db    125  FNPMCRYRLSTLEYDGEEISGLARCPFDARQTNVALFADGKLYSATVADFLASDAVIYR 184

Qy    200  SLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYFFFREIAVEYNTMGKVVPFPRVAQVCK 259
      |:: | ||:|:||||:||||: |::|:|:| ||||| ||| :|| | :||:|
Db    185  SMGDGSALRTIKYDSKWIKEPHFLHAIEYGNVYVFFFREIAVEHNNLGKAVYSRVARICK 244

Qy    260  NDMGGSQRVLEKQWTSFLKARLNCSPVGDSEHYFNILQAVTDVIRINGRDVVLATFSTPY 319
      ||||| ||||| ||||| ||||| ||||:|:|:|:|:| ||| | :|
Db    245  NDMGGSQRVLEKHWTSFLKARLNCSPVGDPFFYFDVLQSITDIIQINGIPTVVGVTTLQL 304

Qy    320  NSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVDPDERVPKPRPGCCAGSSSLERYA 379
      ||||| ||||: | || | |||||:| || || ||:|:| ||||| || |
Db    305  NSIPGSAVCAFSMDIEKVFKGRFKEQKTPDSVWTAVPEDKVPKPRPGCCAKHGLAEAYK 364

Qy    380  TSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRLTKIAVDTAAGPYQNHTVVF 439
      || :||:|:|:|:|:| || | : || | :| ||||| |:| :|||:|:|:|
Db    365  TSIDFPDETLSFIKSHPLMDSAVPPIADEPWFTKTRVRYRLTAISVDHSAGPYQNYTVIF 424

Qy    440  LGSEKGIILKFLARIGNSGF-LNDSLFLLEMSVYNSEKCSYDGVEDKRIMGMQLDRASS 498
      :||| |::| ||: | | ||||: ||: || ||| : |||::: :||: :
Db    425  VGSEAGMVLKVLAKE--TSPFSLNDSVLLEEIEAYNHAKCSAENEEDKKVISLQLDKDHHA 482

Qy    499  LYVAFSTCVIKVPLGRGERHGKCKKTCIASRDPYCGWIKEGGACSHLSPNSRLT----- 552
      |||||:|:|:|:| ||||:| |||:|||||||: : |:| :| |
Db    483  LYVAFSSCIIRIPLSRCERYGSCKKSCIASRDPYCGWLSQ-GSCGRVTPGMLLLTEDFFA 541

Qy    553  -----FEQDIERGNTDGLGDCHNSFVALNGHSSSLPSTTTSDSTAQEGYESRGG-- 602
      :||| | ||| |||| |:::| | | : ||
Db    542  FHNHSAEGYEQDTEFGNTAHLGDCH-----EILPTSTTPD-----YKIFGGPT 584

Qy    603  -----MLD-WKHL-----DSP---DSTDPLGAV 622
      :| | : | | | | :
Db    585  SDMEVSSSSVTTMASIPEITPKVIDTWRPKLTSSRKFFVQDDPNTSDFTDPLSGI 639
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RESULT 6
US-09-254-594-6
; Sequence 6, Application US/09254594
; Patent No. 6566094

```
; GENERAL INFORMATION:
; APPLICANT: KIMURA, Toru
; APPLICANT: KIKUCHI, Kaoru
; TITLE OF INVENTION: NOVEL SEMAPHORIN GENE: SEMAPHORIN Y
; FILE REFERENCE: 0020-4527P
; CURRENT APPLICATION NUMBER: US/09/254,594
; CURRENT FILING DATE: 1999-05-11
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 930
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: ()..()
; OTHER INFORMATION: Tissue Type: Child Brain
; NAME/KEY: misc_feature
; LOCATION: ()..()
; OTHER INFORMATION: Identification Method: P for resulting peptide
US-09-254-594-6
```

```
Query Match          27.9%; Score 1519.5; DB 4; Length 930;
Best Local Similarity 35.9%; Pred. No. 3.2e-135;
Matches 381; Conservative 135; Mismatches 356; Indels 189; Gaps 32;
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```
Qy      6 LLLYFTLLHFAGAGFPEDSEPISISHGNYTKQYPVFGHKPGRNTTQRHRLDIQMIMIMN 65
      ||| :| | | ||:| |:| | | : | : || | : :|
Db     13 LLLLLSLPH-TQAAFPQDPLPLLLISDLQGTSPLSWFRGLEDDAVAAEL-GLDFQRFLTLN 70

Qy     66 GTLYIAARDHIYTVDDIDSHT-EEIYCSKKLTWKSQRQADVDTCRMKGKHKDECHNFIKVL 124
      || :|||||::: |: | : :| |||:| | | :| | :|| | | :|:|:|
Db     71 RTLLVAARDHVSFDLQAEEEGGLVPNKYLTWRSQ--DVENCAVRGKLTDECYNYIRVL 128

Qy    125 LKKNDALFVCGTNAFNPSCRNYKMDTLEPFGDEFSGMARCPYDAKHANVALFADGKLYS 184
      : : | |||:|:| ||:| : :| :| || |||:| | :||:|:| | ||
Db    129 VPWDSQTLACGTNSFSFVCRSYGITSLQOEGEELSGQARCPFDATQSNVAIFAEGSLYS 188

Qy    185 ATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYFFFREIAVEYN 244
      || || | |||:|||| | ||: |:||||:|:|:|:|:|:|:|:|:|:|
Db    189 ATAADFQASDAVVYRSLGPQPFLRSKYDSKWLREPHEFVQALEHGDHVFYFFFREVSVEDA 248

Qy    245 TMGKVVFPRVAQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDSHFYFNILQAVTDVIR 304
      :||| | |||:| | |||| | |: |||| | ||||| | |||:|:| | :
Db    249 RLGKVQFSRVARVCKRDMGGSFRALDRHWTSLFLKLRLNCSVPGDSTFYFDVLQALTGPVN 308

Qy    305 INGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVPDERVPKP 364
      ::|| : | :| | ||||| ||| : :| | |:| |||:| | ||| :||| |
Db    309 LHGRSALFGVFTTQTNISIPGSAVCAFYLDEIERGFEGKFKEQKSLDGAWTPVSEDRVPS 368

Qy    365 RPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRLTKIA 424
      ||| ||| : :| : ||| | ||| |||:| ||| : :| | | | :|:|
Db    369 RPGSCAGVGGAALFSSSRDLPPDVLTFIKAHPLLDPAVPPVTHQP-LLTLTSRALLTQVA 427

Qy    425 VDTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLNDSLFLLEMSVYNSEKCSYDGVED 484
      || |||: | ||:| | | :|| | || | : : |||: |: :|
Db    428 VDGMAPHSNITVMFLGSNDGTVLKVLTPGGRSGG-PEPILLEEIDAYSPARCSGKRTAQ 486
```


; TYPE: PRT
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: ()..()
; OTHER INFORMATION: Tissue Type: Brain
; NAME/KEY: misc_feature
; LOCATION: ()..()
; OTHER INFORMATION: Identification Method: P for resulting peptide
US-09-254-594-3

Query Match 26.2%; Score 1428.5; DB 4; Length 929;
Best Local Similarity 34.0%; Pred. No. 1.5e-126;
Matches 360; Conservative 147; Mismatches 355; Indels 197; Gaps 32;

Qy	6	LLLYFTLLHFAGAGFPEDSEPI	SHGNYTKQYPVFGVGHKPG	RNTTQRHRLDIQMIMIMN	65	
			: :	: : :		
Db	11	LLLLLLSLPQAQTAFPDPIPL	LTSDLGTSFSSWFRGLEDDA	VAAEL-GLDFQRFLTLN	69	
Qy	66	GTLYIAARDHIYTVDIDTSH	T-EEIYCSKKLTWKS	RQADVDTCRMKGKHKDE	CHNFIKVL 124	
		: : : :	: : : :: :	: : :		
Db	70	RTLLVAARDHVFSFDLQAQ	EEGEGLVPNKFLT	WRSQ--DMENCAVRG	KLTDECYNIYRVL 127	
Qy	125	LKKNDALFVCGTNAFN	PSCRNYKMDTLE	PGDEFSGMARCPYDA	KHANVALFADGKLYS 184	
		: : : : :	: : : :: :	: : :		
Db	128	VPWDSQTLLACGTNS	FSPVCRSYGITS	LQQEGEELSGQARCP	FDATQSTVAISAEGSLYS 187	
Qy	185	ATVTDFLAIDAVIY	RSLGESPTLR	TVKHDSKW	LKEPYFVQAVDYG	DIYFFFREIAVEYN 244
		:	: : :	:: : :	: :	
Db	188	ATAADFQASDAV	YRSLGPP	PLRS	AKYDSKW	LREPHFVYALEHGDHVF
						FFLPEKSL-WR 246
Qy	245	T--MGKV	VFP	RAQVCKND	MGG	SQRVLEKQWTS
		: : :	::	: :		
Db	247	TPGLGRVQ	FSRVARVCK	RD	MGGSPRALDR	HWT
						SFLKLR
						LNC
						SVPGD
						STFYFDV
						LSLTGP 306
Qy	303	IRINGRDVVLAT	FSTPYNSIP	GS	SAVCAYDML	DIASVFTGRFKEQ
		: : : :	: :	: :	: :	
Db	307	VNLHGRS	ALFGVFTTQ	TNSIP	GS	SAVCAFYLD
						DDIERGFEGKFKEQ
						RS
						LDGAWTPVSE
						DKVP 366
Qy	363	KPRPGCCAGSS	SLERYATSNE	FPDDTLN	FIKTHPLMDE	AVPSIFNRPWFL
		: : :	:	: :	:	
Db	367	SPRPGSCAGV	GAAALFSS	QDL	PDDVLL	FIKAHPLDPAVPP
						PATHQP-LLTLTS
						RALLTQ 425
Qy	423	IAVDTAAGPYQ	NHTV	VFLGSEKGI	ILKFLARIGN	SGFLNDSLFLE
		: : :	:	: : : :	:	
Db	426	VAVDGMAG	PHRNTTVL	FLGSNDGT	VLKVLPP-GG	QSLGPEPIILEE
						IDAYSHARCS--GK 482
Qy	483	ED----	KRIMG	QLDRASS	SLYVAFST	CVIKVPLGR
		: : : :	:: :	:: :		
Db	483	RSPRAARRI	IGLELDTE	GHRLF	VAFPGCIV	YLSLSRCARHGAC
						Q
						RSCLASLDPYCGW
						HRF 542
Qy	539	GGACSHLSP	NSRLTFEQDIE	-RGNTDGL--	GDCHNSF	VALNGHSSSLLP
		:	:: : : :	:	:	
Db	543	RGCVNIR	GPGG-----	TDVDLTGN	QESMEH	GDCQDG-----
						ATGSQSGPGDS 584
Qy	596	GYESRGGMLD	WKHLLD	SPDST	DPLGAVSS	SHNHQDKKGVIRE
						SYLK
						GHDQLVPV
						TLTLLAIAV 655

Db 585 AY-----GVRRLSPASASRSIPIPLLLACV 610
 Qy 656 ILAFVMGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRRGSMSSVTKLSGLFGDTQSK 715
 || :|| ||: || | || : :|: ||: | : | |
 Db 611 AAALFALGASVSGLLVSCAC--RRAN---RRRSKDIETPGLPRPLSLRSLARLHGGGPEP 664
 Qy 716 DPKP---EAILTPLMHNGKLATPGNTAKMLIKADQHHLDTALPTPESTPTLQQKRKPSR 772
 | | :| || :| | : :| ||||:| | | :
 Db 665 PPPPKDGDAAQTPQLYTTFLPPPEGGSPP-----ELACLPTPETTPPELFPVKHLRAS 715
 Qy 773 GSREWERNQNLINACTKDMPPMGSPVIPTDLP---LRASPSHIPSVVVLPIITQQ---GYQ 826
 | || ||| || | | :| | | | : |
 Db 716 GG-PWEWNQNGNNASEGPRGRGCSAAGGPAPRVLRPPPGCPGQEVETTTLEELLRYL 774
 Qy 827 H-----EYVDQPKMSEVAQMALEDQAATLEYKTIKEHLSSKSPNHGVNLV 871
 | : :| || | || |
 Db 775 HGPQPPRKGEPLASAPFTSRPPASEPGAALFVD-----SSPMR----- 814
 Qy 872 ENLDSLPP-----KVPQREASLGPPGASLSQTGLSKRLEMHHSSSYGVVDYKRSY 920
 | :|| | :| | | :| || :
 Db 815 ---DCVPPLRLDVPPDGKRAAPSGRPALSAPAPRLGVSG-SRRL-----PF 856
 Qy 921 PTNSLTRSHQATTCLKRNNTNSSNSSHLNRNQSFGRGDNPPAPQVRDS--IQVHSSQPSG 978
 || :| || || | :| |
 Db 857 PT-----HRA-----PPGLLTRVPSGGPSRYSGGGPR 883
 Qy 979 QAVTVSRQPSLNAYNSLTRSGLKRTPSLKPVD--PPKPS 1015
 : : | | : || | :| | | : ||:|
 Db 884 HLLYLGR-PDGHGRSLKRVDVKSPKPLPLATPPQPA 921

RESULT 8

US-09-653-274-10

; Sequence 10, Application US/09653274

; Patent No. 6635742

; GENERAL INFORMATION:

; APPLICANT: Boyle, Bryan J

; APPLICANT: Yeung, George Y

; APPLICANT: Arterburn, Matthew C

; APPLICANT: Mize, Nancy K

; APPLICANT: Tang, Y. Tom

; APPLICANT: Liu, Chenghua

; APPLICANT: Drmanac, Radoje T

; TITLE OF INVENTION: Methods and Maaterials Relating to Semaphorin-Like

; TITLE OF INVENTION: Polypeptides and Polynucleotides

; FILE REFERENCE: HYS-23

; CURRENT APPLICATION NUMBER: US/09/653,274

; CURRENT FILING DATE: 2000-08-31

; PRIOR APPLICATION NUMBER: 09/491,404

; PRIOR FILING DATE: 2000-01-10

; NUMBER OF SEQ ID NOS: 13

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 10

; LENGTH: 536

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-653-274-10

Query Match 25.3%; Score 1377.5; DB 4; Length 536;
 Best Local Similarity 49.3%; Pred. No. 4.1e-122;
 Matches 265; Conservative 97; Mismatches 167; Indels 9; Gaps 7;

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Qy      6 LLLYFTLLHFAGAGFPEDSEPISISHGNYTKQYPVFVGHKPGRNTTQRRHRLDIQMIMIMN 65
      ||| :| | | ||:| |: || | | : | | : :|
Db      4 LLLLLSLPH-TQAAFPQDPLPLLLISDLQGTSPLSWFRGLEDDAVAAEL-GLDFQRFLTLN 61

Qy     66 GTLYIAARDHIYTVDIDTSHT-EEIYCSKKLTWKSQRQADVDTCRMKGKHKDECHNFIKVL 124
      || :||||:| : | : :| ||:| : || | :|| ||:|:|:|
Db     62 RTLLVAARDHVFSFDLQAEEEGGLVPNKYLTWRSQ--DVENCAVRGKLTDECYNYIRVL 119

Qy    125 LKKNDALFVCGTNAFNPSCRNYKMDTLEPFGDEFSGMARCPYDAKHANVALFADGKLYS 184
      : : | |||:|:| ||:| : :| | | |||:| | :||:|:| | |
Db    120 VPWDSQTLACGTNSFSPVCRSYGITSLQQEGEELSGQARCPFDATQSNVAIFAEGSLYS 179

Qy    185 ATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYFFFREIAVEYN 244
      || || | ||:| || | ||: | :|||:|:| |||:|:|:|:|:|
Db    180 ATAADFQASDAVVYRSLGPQPPLRS AKYDSKWLREPHFVQALEHGDHVFYFFFREVSVEDA 239

Qy    245 TMGKVVFPRAQVCKNDMGGSQRVLEKQWTSFLKARLNC SVPGDSHFYFNILQAVTDVIR 304
      :|| | ||:| | || | | | :| ||| | | | | | | | | | | :|
Db    240 RLGKVQFSRVARVCKRDMGGSPRALDRHWT SFLKRLNC SVPGDSTFYFDVLQALTGPVN 299

Qy    305 INGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVPDERV PKP 364
      :|| : | :| ||| |||:| : :| | :|||:| | ||| :||| |
Db    300 LHGRSALFGVFTTQ TNSIPGSAVCAFYLDEIERGFEGKFKEQ RSLDGAWTPVSED RVSP 359

Qy    365 RPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRLTKIA 424
      ||| ||| :| : || | || | ||:| ||| : :| | | | :|
Db    360 RPGSCAGVGGAALFSSSRDL PDDVLTFIKAHPLLDPAVPPVTHQP-LLTLTSRALLTQVA 418

Qy    425 VDTAAGPYQNHTVFLGSEKGIILKFLARIGNSGFLNDSL FLEEMSVYNSEKCSYDGVED 484
      || |||: | ||:| || | :|| | | | : : |||: | : :|
Db    419 VDMAGPHSNITVMFLGSNDGTVLKVLT PGGRSGG-PEPILLEEIDAYSPARCSGKRTAQ 477

Qy    485 --KRIMGMLDRASSSLYVAFSTCVIKVPLGR CERH GKCKKTCIASRDPYCGWIKEGG 540
      :||:|:| | :|| | :| || || | :|:|:|:| | | |
Db    478 TARRIIGLELDT EGHRLFVAFSGCIVYLP LSRCARHGACQRSLASQDPYCGWHSSRG 535

```

RESULT 9

US-08-121-713D-58

; Sequence 58, Application US/08121713D

; Patent No. 5639856

; GENERAL INFORMATION:

; APPLICANT: Goodman, Corey S.

; APPLICANT: Kolodkin, Alex L.

; APPLICANT: Matthes, David

; APPLICANT: Bentley, David R.

; APPLICANT: O'Connor, Timothy

; TITLE OF INVENTION: The Semaphorin Gene Family

; NUMBER OF SEQUENCES: 100

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP

; STREET: 268 Bush Street, Suite 3200

```

; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/121,713D
; FILING DATE: 13-SEP-1993
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Osman, Richard A.
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: B94-002-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)343-4341
; TELEFAX: (415) 343-4342
; TELEX:
; INFORMATION FOR SEQ ID NO: 58:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 730 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-121-713D-58

```

```

Query Match          17.8%; Score 969.5; DB 1; Length 730;
Best Local Similarity 34.4%; Pred. No. 5.7e-83;
Matches 244; Conservative 124; Mismatches 224; Indels 117; Gaps 29;

```

```

Qy      8 LYFTLLHFAGAGFPEDSEPISISHGNYTKQYPVFVGHKPGRNTTQR-----HRLDIQMI 61
| : || | : | | | | | | | | | | | | | | | | : ::
Db     11 LLWVALH--AAAWVNDVSP-----KMYVQF-----GEERVQRFLGNESHKDHFKLL 54

Qy     62 MIMNGTLYIAARDHIYTVDID--TSHTEEIYCSKKLTWKSQRQADVDTCRMKGKHKDECHN 119
: : | : || : | : : | || : : | | | : | : || : | |
Db     55 EKDHNSSLVGARNIVYNISLRDLTEFTEQ-----RIEWHSSGAHRELCYLKGKSEDDCQN 109

Qy    120 FIKVLLKKND DALFVCGTNAFNPSCRNYKMDTLEPFGD-----EFSGMARCPYDAKHANV 174
: | : || | : || : : || || : | || : | | | : | :
Db    110 YIRVLAKIDDDRVLICGTNAYKPLCRHYALKD----GDYVVEKEYEGRGLCPFPDPDHNST 165

Qy    175 ALFADGKLYSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYF 234
| : : : | : || || | | | | | | | | | | | | | | : | : | : |
Db    166 AIYSEGQLYSATVADFSGTDPLIYRG-----PLRTERS DLKQLNAPNFVNTMEYNDFIFF 220

Qy    235 FFREIAVEYNTMGKVVFPRVAQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPGD SHFYFN 294
| | | | | | | | | | : : | | : | | : : | | | | : | | | | | | | | | |
Db    221 FFRETAVEYINCGKAIYSRVARVCKHDKGGPHQGGDR-WTSFLKSRNLCSVPGDYPPFYFN 279

Qy    295 ILQAVTDVIRIN-GRDV---VLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPD 350
: | : : | | | | : | : | | | | | | : | | | | | : :
Db    280 EIQSTSDIIEGNYGGQVEKLIYGVFTTPVNSIGGSAVCAFSMKSI LESFDGPFKEQETMN 339

```

Qy 351 STWTPVPPERVPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPW 410
 | | | | : | : | | | | | | | | : | : | : | : | | | | : | | |
 Db 340 SNWLAVPSLKVPEPRPGQCVND-----SRTLDPVSVNFVKSHITLMDEAVPAFFTRPI 391

Qy 411 FLRTMVRYRLTKIAVD---TAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLN----- 461
 : | : : | | | | | | | | : : | : | : : | : | | | :
 Db 392 LIRISLQYRFTKIAVDQQVRTPDG--KAYDVLFIGTDDGKVIKAL----NSASFDSSDTV 445

Qy 462 DSLFLEEMSVYNSEKCSYDGVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRC--ERHG 519
 | : : | : | | | | | | | | : : | | | | : : | | : :
 Db 446 DSVVIEELQVLP-----PGVPVKNLYVVRMDGDDSKLVVVSDEILAIKLHRCGSDKIT 499

Qy 520 KCKKTCIASRDPYCGWIKEGGACSHL-SPN---SRLTFEQDIERGNTDGLGDCHNSFVAL 575
 | : : | : : | | | | | | : : | : | : | | | | : :
 Db 500 NCRE-CVSLQDPYCAWDNVELKCTAVGSPDWSAGKRRFIQNISLGEHKACGGRPQTEIV- 557

Qy 576 NGHSSLLPSTTTSDSTA-----QEGYESRGGMLDWKHLLEDSPDSTDPLGAVSSHNHQ 628
 : | : : | : | : | : | : | : : | | : : | |
 Db 558 ----ASPVPTQPTTKSSGDPVHSIHQAEEFEPE---IDNEIVIGVDDSNVIPNTLAEINHA 610

Qy 629 DKKGVIRESYLKGHDQLVPV----TL-LAI-----AVILAFVMGAVFS 666
 | | : : | : | : | : | : | : | : | : | : | : | :
 Db 611 GSK-----LPSSQEKLPITYAETLTIAIVTSCLGALVVGFISGFLFS 652

RESULT 10

US-08-835-268-58

; Sequence 58, Application US/08835268

; Patent No. 5807826

; GENERAL INFORMATION:

; APPLICANT: Goodman, Corey S.

; APPLICANT: Kolodkin, Alex L.

; APPLICANT: Matthes, David

; APPLICANT: Bentley, David R.

; APPLICANT: O'Connor, Timothy

; TITLE OF INVENTION: The Semaphorin Gene Family

; NUMBER OF SEQUENCES: 100

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP

; STREET: 268 Bush Street, Suite 3200

; CITY: San Francisco

; STATE: CA

; COUNTRY: USA

; ZIP: 94104

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/835,268

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/121,713

; FILING DATE: 13-SEP-1993

; ATTORNEY/AGENT INFORMATION:

Db 500 NCRE-CVSLQDPYCAWDNVELKCTAVGSPDWSAGKRRFIQNISLGEHKACGGRPQTEIV- 557

Qy 576 NGHSSLLPSTTTSDSTA-----QEGYESRGGMLDWKHLLDSPDSTDPLGAVSSSHNHQ 628
 :| :|: |: |: | :| :| :| :|: || :| :|

Db 558 ----ASPVPTQPTTKSSGDPVHSIHQAEFEPE---IDNEIVIGVDDSNVIPNTLAEINHA 610

Qy 629 DKKGVIRESYLKGHDLVLPV----TL-LAI-----AVILAFVMGAVFS 666
 | :|: || :|| |:: |: | :||

Db 611 GSK-----LPSSQEKLPITYAETLTIAIVTSCILGALVVGFI SGFLFS 652

RESULT 11

US-09-060-692-58

; Sequence 58, Application US/09060692

; Patent No. 5935865

; GENERAL INFORMATION:

; APPLICANT: Goodman, Corey S.

; APPLICANT: Kolodkin, Alex L.

; APPLICANT: Matthes, David

; APPLICANT: Bentley, David R.

; APPLICANT: O'Connor, Timothy

; TITLE OF INVENTION: The Semaphorin Gene Family

; NUMBER OF SEQUENCES: 100

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP

; STREET: 268 Bush Street, Suite 3200

; CITY: San Francisco

; STATE: CA

; COUNTRY: USA

; ZIP: 94104

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/060,692

; FILING DATE:

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/121,713

; FILING DATE: 13-SEP-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Osman, Richard A.

; REGISTRATION NUMBER: 36,627

; REFERENCE/DOCKET NUMBER: B94-002-1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 343-4341

; TELEFAX: (415) 343-4342

; TELEX:

; INFORMATION FOR SEQ ID NO: 58:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 730 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-09-060-692-58

Query Match 17.8%; Score 969.5; DB 2; Length 730;
 Best Local Similarity 34.4%; Pred. No. 5.7e-83;
 Matches 244; Conservative 124; Mismatches 224; Indels 117; Gaps 29;

Qy	8	LYFTLLHFAGAGFPEDSEPISISHGNYTKQYPVFVGHKPGRNNTQR-----HRLDIQMI	61
		: : : ::	
Db	11	LLWVALH--AAAWVNDVSP-----KMYVQF-----GEERVQRFLGNESHKDHFKLL	54
Qy	62	MIMNGTLYIAARDHIYTVDID--TSHTEEIYCSKKLTWKSQRQADVDTCRMKGKHKDECHN	119
		: : : : : : : : : : :	
Db	55	EKDHNSSLVGARNIVYNISLRDLTEFTEQ-----RIEWHSSGAHRELCYLKGKSEDDCQN	109
Qy	120	FIKVLKKNDALFVCGTNAFNPSRCRNYKMDTLEPFGD-----EFSGMARCPYDAKHANV	174
		: : : : : : : : : :	
Db	110	YIRVLAKIDDDRVLICGTNAYKPLCRHYALKD----GDYVVEKEYEGRGLCPFPDPHNST	165
Qy	175	ALFADGKLYSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYF	234
		: : : : : : : : :	
Db	166	AIYSEGLYSATVADFSGTDLPIYRG-----PLRTERSCLKQLNAPNFVNTMEYNDFIFF	220
Qy	235	FFREIAVEYNTMGKVVFPRVAQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDSHFYFN	294
		: : : : : : : :	
Db	221	FFRETAVEYINCGKAIYSRVARVCKHKDGPHQGGDR-WTSFLKSRLNCSVPGDYPFYFN	279
Qy	295	ILQAVTDVIRIN-GRDV---VLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPD	350
		: : : : : : : : : :	
Db	280	EQSTSDIIEGNYGGQVEKLIYGVFTTPVNSIGGSAVCAFSMKSILESFDGPFKEQETMN	339
Qy	351	STWTPVPDERVPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPW	410
		: : : : : :	
Db	340	SNWLAVPSLKVPEPRPGQCVND-----SRTLDPVSVNFVKSHTLMDEAVPAFFTRPI	391
Qy	411	FLRTMVRYRLTKIAVD----TAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLN-----	461
		: : : : : : : : : : :	
Db	392	LIRISLQYRFTKIAVDQQVVRTPDG--KAYDVLFIGTDDGKVIKAL----NSASFDSSDTV	445
Qy	462	DSLFLEEMSVYNSEKCSYDGVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRC--ERHG	519
		: : : : : : : : : : :	
Db	446	DSVVIEELQVLP-----PGVPVKNLVVRMDGDDSKLVVVSDDDEILAIKLHRCGSDKIT	499
Qy	520	KCKKTCIASRDPYCGWIKEGGACSHL-SPN---SRLTFEQDIERGNTDGLGDCHNSFVAL	575
		: : : : : : : : : :	
Db	500	NCRE-CVSLQDPYCAWDNVELKCTAVGSPDWSAGKRRFIQNISLGEHKACGGRPQTEIV-	557
Qy	576	NGHSSSLLPSTTTSDSTA-----QEGYESRGGMLDWKHLSDSPDSTDPLGAVSSHNHQ	628
		: : : : : : : : : : :	
Db	558	----ASPVPTQPTTKSSGDPVHSIHQAEFEPE---IDNEIVIGVDDSNVIPNTLAEINHA	610
Qy	629	DKKGVIRESYLKGHDLVPV----TL-LAI-----AVILAFVMGAVFS	666
		: : : : : : :	
Db	611	GSK-----LPSSQEKLPIYTAETLTIAIVTSCLGALVVGFI SGFLFS	652

RESULT 12
 US-08-833-391-58
 ; Sequence 58, Application US/08833391

```

; Patent No. 6013781
; GENERAL INFORMATION:
;   APPLICANT: Goodman, Corey S.
;   APPLICANT: Kolodkin, Alex L.
;   APPLICANT: Matthes, David
;   APPLICANT: Bentley, David R.
;   APPLICANT: O'Connor, Timothy
;   TITLE OF INVENTION: The Semaphorin Gene Family
;   NUMBER OF SEQUENCES: 100
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
;     STREET: 268 Bush Street, Suite 3200
;     CITY: San Francisco
;     STATE: CA
;     COUNTRY: USA
;     ZIP: 94104
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/833,391
;     FILING DATE:
;     CLASSIFICATION: 530
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US 08/121,713
;     FILING DATE: 13-SEP-1993
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Osman, Richard A.
;     REGISTRATION NUMBER: 36,627
;     REFERENCE/DOCKET NUMBER: B94-002-1
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (415)343-4341
;     TELEFAX: (415) 343-4342
;     TELEX:
;   INFORMATION FOR SEQ ID NO: 58:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 730 amino acids
;       TYPE: amino acid
;       TOPOLOGY: linear
;     MOLECULE TYPE: protein
US-08-833-391-58

```

```

Query Match          17.8%; Score 969.5; DB 3; Length 730;
Best Local Similarity 34.4%; Pred. No. 5.7e-83;
Matches 244; Conservative 124; Mismatches 224; Indels 117; Gaps 29;

```

```

Qy      8 LYFTLLHFAGAGFPEDSEPISISHGNYTKQYPVFVGHKPGRNNTQR-----HRLDIQMI 61
      | : || | : | | | | | | | | | | | | | | | | : ::
Db     11 LLWVALH--AAAWVNDVSP-----KMYVQF-----GEERVQRFLGNESHKDHFKLL 54

Qy     62 MIMNGTLYIAARDHIYTVDID--TSHTEEIYCSKKLTWKSQRQADVDTCRMKGKHKDECHN 119
      : : | : || : | : : | || : : | | | : | : || : | |
Db     55 EKDHNSSLVGARNIVYNISLRDLTEFTEQ-----RIEWHSSGAHRELCYLKGKSEDDCQN 109

Qy    120 FIKVLLKKNDALFVCGTNAFNPSCRNYKMDTLEPFGD-----EFSGMARCPYDAKHANV 174

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      :|:| | :| : :| | | : | | : | : | : | : | :
Db      110 YIRVLAKIDDDRVLICGTNAYKPLCRHYALKD----GDYVVEKEYEGRGLCPFDPDHNS 165

Qy      175 ALFADGKLYSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYF 234
      |:::|:| | | | | | | | | :| | | | | | :| | :| | :|
Db      166 AIYSEGQLYSATVADFSGTDPLIYRG-----PLRTERSCLKQLNAPNFVNTMEYNDFIFF 220

Qy      235 FFREIAVEYNTMGKVVFPRVAQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDSHFYFN 294
      | | | | | | | | :| :| :| :| :| | : :| :| :| :| :| :| :|
Db      221 FFRETAVEYINCGKAIYSRVARVCKHDKGGPHQGGDR-WTSFLKSRLNCSVPGDYPFYFN 279

Qy      295 ILQAVTDVIRIN-GRDV---VLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPD 350
      :| :| :| | | | : | :| | | | | | :| | | | | :| :| :| :|
Db      280 EIQSTSDIIEGNYGGQVEKLIYGVFTTPVNSIGGSAVCAFSMKSILESFDGPFKEQETMN 339

Qy      351 STWTPVPDERVVKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPW 410
      | | | | :| :| | | | | | | | :| :| :| :| | | | | :| | |
Db      340 SNWLAVPSLVPEPRPGQCVND-----SRTLDPVSVNFVKSHTLMDEAVPAFFTRPI 391

Qy      411 FLRTMVRYRLTKIAVD----TAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLN----- 461
      :| :| :| | | | | | | :| :| :| :| :| :| :| :| :| :| :|
Db      392 LIRISLQYRETKIAVDQQVTPDG--KAYDVLFIGTDDGKVIKAL----NSASFSSDTV 445

Qy      462 DSLFLEEMSVYNSEKCSYDGVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRC--ERHG 519
      | | :| :| | | | | | | :| :| :| :| | | :| :| :| :| :|
Db      446 DSVVIEELQVLP-----PGVPVKNLYVVRMDGDDSKLVVSDDEILAIKLHRCGSDKIT 499

Qy      520 KCKKTCIASRDPYCGWIKEGGACSHL-SPN---SRLTFEQDIERGNTDGLGDCHNSFVAL 575
      | :| :| :| | | | | :| :| | :| :| :| :| :| :| :| :|
Db      500 NCRE-CVSLQDPYCAWDNVELKCTAVGSPDWSAGKRRFIQNISLGEHKACGGRPQTEIV- 557

Qy      576 NGHSSSLLPSTTTSDSTA-----QEGYESRGGMLDWKHLDDSPDSTDPLGAVSSHNHQ 628
      :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db      558 ----ASPVPTQPTTKSSGDPVHSIHQAEFEPE---IDNEIVIGVDDSNVIPNTLAEINHA 610

Qy      629 DKKGVIRESYLKGHDLQVLPV----TL-LAI-----AVILAFVMGAVFS 666
      | | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db      611 GSK-----LPSSQEKLPITYAETLTIAIVTSCLGALVVGFI SGFLFS 652

```

RESULT 13

US-09-060-610-58

; Sequence 58, Application US/09060610

; Patent No. 6344544

; GENERAL INFORMATION:

; APPLICANT: Goodman, Corey S.

; APPLICANT: Kolodkin, Alex L.

; APPLICANT: Matthes, David

; APPLICANT: Bentley, David R.

; APPLICANT: O'Connor, Timothy

; TITLE OF INVENTION: The Semaphorin Gene Family

; NUMBER OF SEQUENCES: 100

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP

; STREET: 268 Bush Street, Suite 3200

; CITY: San Francisco

; STATE: CA

```

; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/060,610
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/835,268
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Osman, Richard A.
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: B94-002-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)343-4341
; TELEFAX: (415) 343-4342
; TELEX:
; INFORMATION FOR SEQ ID NO: 58:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 730 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-060-610-58

```

```

Query Match          17.8%; Score 969.5; DB 4; Length 730;
Best Local Similarity 34.4%; Pred. No. 5.7e-83;
Matches 244; Conservative 124; Mismatches 224; Indels 117; Gaps 29;

```

```

Qy      8 LYFTLLHFAGAGFPEDSEPISISHGNYTKQYPVFVGHKPGRNNTTQR-----HRLDIQMI 61
      | : || | : | | | | | | | | | | | | | | | | : ::
Db     11 LLWVALH--AAAWVNDVSP-----KMYVQF-----GEERVQRFLGNESHKDHFKLL 54

Qy     62 MIMNGTLYIAARDHIYTVDID--TSHTEEIYCSKKLTWKSQRQADVDTCRMKGKHKDECHN 119
      : : | : || : | : : | || : : : | | | : | : || : | : |
Db     55 EKDHNSLLVGARNIVYNISLRDLTEFTEQ-----RIEWHSSGAHRELCYLKGKSEDDCQN 109

Qy    120 FIKVLLKKNDALFVCGTNAFNPSCRNYKMDTLEPFGD-----EFGSMARCPYDAKHANV 174
      : | : || | : || : : || || : | || : | | : | : || | : |
Db    110 YIRVLAKIDDDRVLICGTNAYKPLCRHYALKD----GDYVVEKEYEGRGLCPFDPDHNST 165

Qy    175 ALFADGKLYSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYF 234
      | : : : | : || || | | | : || | || : | | | | | | : | | : |
Db    166 AIYSEGQLYSATVADFSGTDPLIYRG-----PLRTERSCLKQLNAPNFVNTMEYNDFIFF 220

Qy    235 FFREIAVEYNTMGKVVFPRVAQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDSHFYFN 294
      || || | || | || : : || : || : | : : : || || : || || || || ||
Db    221 FFRETAVEYINCGKAIYSRVARVCKHDKGGPHQGGDR-WTSFLKSRLNCSVPGDYPFYFN 279

Qy    295 ILQAVTDVIRIN-GRDV---VLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPD 350
      : : : : | | | : | : || || || || : | | | | || : :
Db    280 EIQSTSDIIEGNYGGQVEKLIYGVFTTPVNSIGGSAVCAFSMKSIKSFDFGPFKEQETMN 339

```

Qy 351 STWTPVPPERVPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPW 410
 | | | | : | : | | | | | | | | : | : | : | : | | | | | : | | |
 Db 340 SNWLAVPSLVPEPRPGQCVND-----SRTLPDVSVNFVKSHTLMDPAFFTRPI 391

Qy 411 FLRTMVRYRLTKIAVD----TAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLN----- 461
 : | : : | | | | | | | | : : | : | : | : | : | : | : | : | :
 Db 392 LIRISLQYRFTKIAVDQQVRTPDG--KAYDVLFIGTDDGKVIKAL----NSASFDSSDTV 445

Qy 462 DSLFLEEMSVYNSEKCSYDGVEDKRIMGMLDRASSSLYVAFSTCVIKVPLGRC--ERHG 519
 | : : | : | | | | | | : : | : | : | : | : | : | : | : | :
 Db 446 DSVVIEELQVLP-----PGVPVKNLYVVRMDGDDSKLVVVSDEILAIKLRHRCGSDKIT 499

Qy 520 KCKKTCIASRDPYCGWIKEGGACSHL-SPN---SRLTFEQDIERGNTDGLGDCHNSFVAL 575
 | : : | : : | | | | | | : : | : | : | : | : | : | : | : | :
 Db 500 NCRE-CVSLQDPYCAWDNVELKCTAVGSPDWSAGKRRFIQNISLGEHKACGGRPQTEIV- 557

Qy 576 NGHSSLLPSTTTSDSTA-----QEGYESRGGMLDWKHLDDSPDSTDP LGAVSSHNHQ 628
 : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
 Db 558 ----ASPVPTQPTTKSSGDPVHSIHQAEEFEPE---IDNEIVIGVDDSNVIPNTLAEINHA 610

Qy 629 DKKGVIRESYLKGHDQLVPV----TL-LAI-----AVILAFVMGAVFS 666
 | | | : : | : | : | : | : | : | : | : | : | : | : | : | :
 Db 611 GSK-----LPSSQEKLPIYTAETLTIAIVTSCLGALVVGFI SGFLFS 652

RESULT 14

PCT-US94-10151A-58

; Sequence 58, Application PC/TUS9410151A

; GENERAL INFORMATION:

; APPLICANT: The Regents of the University of California

; TITLE OF INVENTION: The Semaphorin Gene Family

; NUMBER OF SEQUENCES: 66

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: FLEHR HOHBACH TEST ALBRITTON & HERBERT

; STREET: 4 Embarcadero Center, Suite 3400

; CITY: San Francisco

; STATE: CA

; COUNTRY: USA

; ZIP: 94111-4187

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US94/10151A

; FILING DATE: 13-SEP-1994

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Osman, Richard A.

; REGISTRATION NUMBER: 36,627

; REFERENCE/DOCKET NUMBER: FP-58750-PC/RAO

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 781-1989

; TELEFAX: (415) 398-3249

; TELEX: 910 277299 FHT UR

```
; INFORMATION FOR SEQ ID NO: 58:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 730 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
PCT-US94-10151A-58
```

```
Query Match          17.8%; Score 969.5; DB 5; Length 730;
Best Local Similarity 34.4%; Pred. No. 5.7e-83;
Matches 244; Conservative 124; Mismatches 224; Indels 117; Gaps 29;
```

```
Qy      8 LYFTLLHFAGAGFPEDESEPI SISHGNYTKQYPVFVGHKPGRNTTQR-----HRLDIQMI 61
      | : || | : | | | | | | | | | | | | | | | | : ::
Db     11 LLWVALH--AAAWVNDVSP-----KMYVQF-----GEERVQRFLGNESHKDHFKLL 54

Qy     62 MIMNGTLYIAARDHIYTVDDID--TSHTEEIYCSKKLTWKSQRQADVDCRMKGKHKDECHN 119
      : : | : || : | : : | || : : | | | : | : || : | : |
Db     55 EKDHNSLLVGARNIVYNISLRDLTEFTEQ-----RIEWHSSGAHRELCYLKKGKSEDDCQN 109

Qy    120 FIKVLLKKNDDALFVCGTNAFNPSCRNYKMDTLEPFGD-----EFSGMARCPYDAKHANV 174
      : : || | : || : : || || : | || : | | : | || : | :
Db    110 YIRVLAKIDDDRVLICGTNAYKPLCRHYALKD----GDYVVEKEYEGRGLCPFPDPDHNST 165

Qy    175 ALFADGKLYSATVTDFLAIDAVIYRSLGESPTLRVTKHDSKWLKEPYFVQAVDYGDIYIF 234
      | : : : | : || || | | | : || | || : | | | | | | : : | | : | :
Db    166 AIYSEGQLYSATVADFSGTDPLIYRG-----PLRTERSCLKQLNAPNFVNTMEYNDFIFF 220

Qy    235 FFREIAVEYNTMGKVVFPRVAQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDSHFYFN 294
      || || || || | | : : || : || : | | : : || || : || || || || || || ||
Db    221 FFRETAVEYINCGKAIYSRVARVCKHDKGGPHQGGR-WTSFLKSRLNCSVPGDYPFYFN 279

Qy    295 ILQAVTDVIRIN-GRDV---VLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPD 350
      : | : : | | | | : | : || || || || || : | | | | || : : :
Db    280 EIQTSDIIEGNYGGQVEKLIYGVFTTPVNSIGGSAVCAFSMKSILESFDGPFKEQETMN 339

Qy    351 STWTPVPDERVPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPW 410
      | | || : || : || | | | | | | | | : || : || : || : || : ||
Db    340 SNWLAVPSLKVPEPRPGQCVND-----SRTLDPVSVNFVKSHTLMDEAVPAFFTRPI 391

Qy    411 FLRTMVRYRLTKIAVD----TAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLN----- 461
      : | : : || || || | | : : | : | : : | : | | | :
Db    392 LIRISLQYRFTKIAVDQQVRTPDG--KAYDVLFIGTDDGKVIKAL----NSASFDSSDTV 445

Qy    462 DSLFLEEMSVYNSEKCSYDGVEDKRIMGMLDRASSSLYVAFSTCVIKVPLGRC--ERHG 519
      || : : || : | | | : : : | | | : : : | | | : :
Db    446 DSVVIEELQVLP-----PGVPVKNLVVRMDGDDSKLVVVSDDDEILA IKLHRCGSDKIT 499

Qy    520 KCKKTCIASRDPYCGWIKEGGACSHL-SPN---SRLTFEQDIERGNTDGLGDCHNSFVAL 575
      | : | : : || || | | : : || : | : | | | : :
Db    500 NCRE-CVSLQDPYCAWDNVELKCTAVGSPDWSAGKRRFIQNISLGEHKACGGRPQTEIV- 557

Qy    576 NGHSSSLLPSTTTSDSTA-----QEGYESRGGMLDWKHLDSPDSTDPLGAVSSSHNHQ 628
      : | : : | : | : | : | : : : || : : ||
Db    558 ----ASPVPTQPTTKSSGDPVHSIHQAEFEPE---IDNEIVIGVDDSNVIPNTLAEINHA 610

Qy    629 DKKGVIRESYLKGHDLQVLPV----TL-LAI-----AVILAFVMGAVFS 666
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Db 611 GSK-----LPSSQEKLPITYTAETLTIAIVTSCLGALVVGFI SGFLFS 652

RESULT 15

US-08-121-713D-60

; Sequence 60, Application US/08121713D

; Patent No. 5639856

; GENERAL INFORMATION:

; APPLICANT: Goodman, Corey S.

; APPLICANT: Kolodkin, Alex L.

; APPLICANT: Matthes, David

; APPLICANT: Bentley, David R.

; APPLICANT: O'Connor, Timothy

; TITLE OF INVENTION: The Semaphorin Gene Family

; NUMBER OF SEQUENCES: 100

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP

; STREET: 268 Bush Street, Suite 3200

; CITY: San Francisco

; STATE: CA

; COUNTRY: USA

; ZIP: 94104

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/121,713D

; FILING DATE: 13-SEP-1993

; CLASSIFICATION: 514

; ATTORNEY/AGENT INFORMATION:

; NAME: Osman, Richard A.

; REGISTRATION NUMBER: 36,627

; REFERENCE/DOCKET NUMBER: B94-002-1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415)343-4341

; TELEFAX: (415) 343-4342

; TELEX:

; INFORMATION FOR SEQ ID NO: 60:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 650 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-121-713D-60

Query Match 16.1%; Score 880; DB 1; Length 650;

Best Local Similarity 35.8%; Pred. No. 1.6e-74;

Matches 207; Conservative 95; Mismatches 194; Indels 82; Gaps 19;

Qy 114 KDECHNFIKVLKKNDDALFVCGTNAFNPSCRNYKMD----TLEPFGDEFSGMARCPYDA 169
:|:| |:|::: : |||||:| | | : ||| :| | |||

Db 1 EDDCQNYIRIMVVPSPGRLFVCGTNSFRPMCNTYIISDSNYTLEA---TKNGQAVCPYDP 57

Qy 170 KHANVALFADGKLYSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYG 229

```

      :| : :: || :||| || || | :||| | :| ::|| | | || : |
Db      58 RHNSTSVLADNELYSGTVADFGSDPIIYRE-----PLQTEQYDSLNLNAPNFVSSFTQG 112

Qy      230 DYIYFFFREIAVEYNTMGKVVFPFVAQVCKNDMGGSQVRVLEKQWTSFLKARLNCSVPGDS 289
      |:|:||||| |||: || :: |||:||| | || | :|:||||:|||||:||||
Db      113 DFVYFFFRETAVEFINCGKAIYSRVARVCKWDKGGPHR-FRNRWTSFLKSRLNCSIPGDY 171

Qy      290 HFYFNILQAVTDVIR----INGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKE 345
      |||| :|: :::: :: |:|| |||||:|: : ||| | |:|||
Db      172 PFYFNEIQSASNLVEGQYGSMSKLIYGVFNTSPNSIPGSAVCAAFALQDIADTFEGQFKE 231

Qy      346 QKSPDSTWTPVPDERVPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSI 405
      | :| | || : :|| |||| | : | || ||||| |||| ||:
Db      232 QTGINSNWLPVNNAKVPDPRPGSC-----HNDSRALPDPTLNFIKTHSLMDENVPAF 283

Qy      406 FNRPFWFLRTMVRYRLTKIAVD----TAAGPYQNHTVVFLGSEKGIILKFL-ARIGNSGFL 460
      |:| :|| || |:|||| | | : : |:|:|:| | |:| : | :|
Db      284 FSQPILVRTSTIYRFTQIAVDAQIKTPGG--KTYDVIFVGTDHGKIIKSVNAESADSADK 341

Qy      461 NDSLFLLEMSVYNSEKCSYDGVEDKRIM-GMQLDRASSSLY-----VAFSTCVIKVPLG 513
      |: :||: | : : : |: || |: | : : |: : |
Db      342 VTSVVIEEIDVLTKS----EPIRNLEIVRTMQYDQPKDGSYDDGKLIIVTDSQVVAIQ LH 397

Qy      514 RC--ERHGKCKKTCIASRDPYCGWIKGGAC-SHLSPN--SRLTFEQDIERGNTDGLGDC 568
      || :: | : |:| :|||| | | | || :| | |:| |
Db      398 RCHNDKITSCSE-CVALQDPYCAWDKIAGKCRSHGAPRWLEENYFYQNVATGQ----- 449

Qy      569 HNSFVALNGHSSSLPSTTTSDSTAQEGYESRGGMLDWKHLLDSPDSTDPLGAVSSH NHQ 628
      |:: : |: | | | | |||| |
Db      450 -----HAACPSGKINSKDANAGEQKGFRNDM----DLLDS-----RRQ 483

Qy      629 DKKGVIRESYLKGHDLVPVTLLAIAVILAFVMGAVFS 666
      | | :: | : :: ::| : |:| |
Db      484 SKDQEIIDNIDKNFEDIINAQYTVETLMAVLAGSIFS 521

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Search completed: March 24, 2004, 13:17:59
Job time : 36.7132 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 24, 2004, 13:11:23 ; Search time 30.8439 Seconds
(without alignments)
3212.214 Million cell updates/sec

Title: US-09-856-681A-2
Perfect score: 5450
Sequence: 1 MRSEALLLYFTLLHFAGAGF.....PPKPSFAPLSTSMKPNDACT 1030

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	971.5	17.8	730	2	JH0798	fasciclin IV precu
2	875	16.1	656	2	B49423	semaphorin I - fru
3	852.5	15.6	771	2	D49423	semaphorin III pre
4	845.5	15.5	711	2	A49423	semaphorin I precu
5	842.5	15.5	772	2	I48747	semaphorin D - mou
6	839.5	15.4	772	2	A49069	collapsin - chicke
7	830	15.2	1074	2	JC5928	semaphorin F precu
8	826	15.2	749	2	G01856	semaphorin V - hum
9	803	14.7	748	2	I48744	semaphorin A - mou
10	793.5	14.6	666	2	I58169	semaphorin III - m
11	789	14.5	712	2	T27165	hypothetical prote
12	779.5	14.3	724	2	C49423	semaphorin II prec
13	768	14.1	753	2	G02173	semaphorin III fam

14	737	13.5	751	2	I48748	semaphorin E - mou
15	692	12.7	834	2	S66498	M-sema F protein p
16	656	12.0	782	2	I48746	semaphorin C - mou
17	641.5	11.8	760	2	I48745	semaphorin B - mou
18	356.5	6.5	653	2	T03102	semaphorin homolog
19	322.5	5.9	676	2	T33853	hypothetical prote
20	238	4.4	1945	2	T13937	plexin A - fruit f
21	217	4.0	403	2	E42521	A39R protein - vac
22	208	3.8	441	2	S29921	hypothetical prote
23	199.5	3.7	1884	2	JC4975	plexin 2 precursor
24	182	3.3	1905	2	I51553	Plexin - African c
25	163.5	3.0	3968	2	A44265	trithorax homolog
26	158	2.9	2051	2	T13164	plexin B - fruit f
27	155.5	2.9	1894	2	JC4980	plexin 1 precursor
28	155	2.8	1375	1	JC5148	hepatocyte growth
29	155	2.8	2352	2	T30201	Notch homolog prot
30	153	2.8	625	2	S48941	regulatory protein
31	147.5	2.7	3507	2	T34513	hypothetical prote
32	147	2.7	1425	2	T30811	hepatocyte growth
33	146.5	2.7	295	2	JQ1775	SalL9R protein - v
34	140	2.6	1390	1	TVHUME	hepatocyte growth
35	139.5	2.6	3869	2	A48205	All-1 protein +GTE
36	138.5	2.5	1065	2	S19482	hypothetical prote
37	138	2.5	728	2	S48569	hypothetical prote
38	137	2.5	867	2	T41308	hypothetical zinc-
39	137	2.5	2492	1	C44213	nonstructural poly
40	136.5	2.5	1347	2	T02214	ubiquitous TPR mot
41	136	2.5	1310	2	T40135	oxysterol-binding
42	136	2.5	2531	2	S18188	notch protein homo
43	133.5	2.4	1829	2	T14280	RW1 protein - mous
44	133.5	2.4	2187	2	T30826	nascent polypeptid
45	133.5	2.4	2531	2	A46019	notch-1 protein -

ALIGNMENTS

RESULT 1

JH0798

fasciclin IV precursor - American bird grasshopper

C;Species: Schistocerca americana (American bird grasshopper)

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999

C;Accession: JH0798

R;Kolodkin, A.; Matthes, D.J.; O'Connor, T.P.; Patel, N.H.; Admon, A.; Bentley, D.; Goodman, C.S.

Neuron 9, 831-845, 1992

A;Title: Fasciclin IV: Sequence, expression, and function during growth cone guidance in the grasshopper embryo.

A;Reference number: JH0798; MUID:93040225; PMID:1418998

A;Accession: JH0798

A;Molecule type: mRNA

A;Residues: 1-730 <KOL>

A;Cross-references: GB:L00709; NID:g160844; PID:g160845

A;Experimental source: embryo

C;Comment: This protein plays a role in growth cone guidance in the developing central nervous system.

C;Keywords: glycoprotein; transmembrane protein

F;1-22/Domain: signal sequence #status predicted <SIG>
 F;23-730/Product: fasciclin IV #status predicted <MAT>
 F;23-627/Domain: extracellular #status predicted <EXT>
 F;628-652/Domain: transmembrane #status predicted <TMM>
 F;653-730/Domain: intracellular #status predicted <INT>
 F;44,71,163,267,360,539/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 17.8%; Score 971.5; DB 2; Length 730;
 Best Local Similarity 34.4%; Pred. No. 5.7e-57;
 Matches 244; Conservative 124; Mismatches 224; Indels 117; Gaps 29;

Qy	8	LYFTLLHFAGAGFPEDSEPI	SHGN	YTKQYP	VFVGHK	PGRN	TTQR-----	HRLDIQMI	61			
		: :					: ::					
Db	11	LLWVALH--AAAWVNDVSP-----	KMYVQF-----	GEERVQ	RFLGNESH	KDHF	KLL	54				
Qy	62	MIMNGTLYIAARDHIY	TVDDI--	TSHT	EIYCSK	KLTK	WSRQAD	VDTCRM	KGKHKDECHN	119		
		: : : : :	:	:		: : : :						
Db	55	EKDHNSLLVGARNIVYNIS	LRDLTE	FTEQ----	RIEWHSS	GAHREL	CYLKGK	SEDDCQN	109			
Qy	120	FIKVLKKNDALFVCGT	NAFNP	SCRNYK	MDTLE	PFPGD----	EFSGMAR	CPYDAKHANV	174			
		: : : : : :	:	:		: : :						
Db	110	YIRVLAKIDDDRVLICGT	NAYKPL	CRHYAL	KD----	GDYVVE	KEYEGR	GLCPFD	PDHNST	165		
Qy	175	ALFADGKLYSATVTDF	LAI	DAVIYR	SLGES	PTLR	TVKHDS	KWLKEPYF	VQAVDYGDYIYF	234		
		: : : :	:	:	:		:	: : :				
Db	166	AIYSEGQLYSATVADFS	GTDP	LIYRG----	PLRTERS	DLKQLN	APNFVN	TMEYND	FIF	220		
Qy	235	FFREIAVEYNTMGKV	VFPR	VAQVCK	NDMGGS	QRVLE	KQWTS	SFLKAR	LNC	SVPGDSHFYFN	294	
			:	: : :	:	:						
Db	221	FFRETAVEYINCGKAI	YSRVAR	VCKHDK	GGPHQ	FGDR--	WTSFLK	SRLNCS	VP	PGDYPFYFN	279	
Qy	295	ILQAVTDVIRIN-GRDV--	VLATF	STPYN	SIPGSA	VCAYDM	LDIASV	FTGR	FKEQKSPD	350		
		: : :	:	: :	:	:	:					
Db	280	EIQSTSDIIEGNYGGQ	VEKLI	YGVFT	TPVNSI	GGSAV	CAFSMKS	ILES	SF	DGPFKEQETMN	339	
Qy	351	STWTPVPDERVPKPR	PGCCAG	SSSL	ERYAT	SNEFP	DDTLN	FIKTH	PLMDEAV	PSIFNRPW	410	
		: :		:	: : : :							
Db	340	SNWLAVPSLKVPEPR	PGQCV	ND-----	SRTL	PDVSVN	FKSHTL	MDEAVE	AF	FTTRPI	391	
Qy	411	FLRTMVRYRLTKIAVD--	TAAG	PYQN	HTVVF	L	GSEKGI	LKFLAR	IGNSGFLN-----	461		
		: : :	:	: : : : :	:		:					
Db	392	LIRISLQYRFTKIAVD	QQV	RTPDG--	KAYD	VLFI	GTDDGK	VIKAL----	NSAS	FDSSDTV	445	
Qy	462	DSLFL	EEMSVYNSEK	CSYD	GVEDK	RIMGM	QLDR	ASSLY	VAFST	CVIKVPLGRC--	ERHG	519
		: :	:	: : :	:	:	:	:	:	:		
Db	446	DSVVIEELQVLP-----	PGVP	VKNLY	VVRMD	GDDSK	L	VVSD	DEILAI	KLHRCGSDKIT	499	
Qy	520	KCKKTCIASRDPYCG	WIEKG	GACSHL-SPN---	SRLT	FEQDI	ERGNTD	GLGD	CHNSFVAL	575		
		: : : :	: :	: :	:	:		:	:			
Db	500	NCRE-CVSLQDPYCA	WDNVEL	KCTAV	GSPD	WSAGK	RRFIQ	NISL	GEHKAC	GGRPQTEIV-	557	
Qy	576	NGHSSSLPSTTTSD	STA-----	QEGY	ESRGG	MLDWK	HL	LDSP	STDPL	GAVSSSHNHQ	628	
		: : : : :	: :	: :	:	: : :		:	:			
Db	558	----ASPVPTQPTTK	SSGDP	VHSIH	QAEFE	PE---ID	NEIV	IGVDD	SNVIP	NTLAEINHA	610	
Qy	629	DKKGV	IRESYLK	GHDQL	VPV----	TL-LAI-----	AVILA	FVMG	AVFS	666		

Db 611 GSK-----LPSSQEKLPITYTAETLTIAIVTSCLGALVVGFI SGFLFS 652

RESULT 2

B49423

semaphorin I - fruit fly (*Drosophila melanogaster*) (fragment)

C;Species: *Drosophila melanogaster*

C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 07-May-1999

C;Accession: B49423

R;Kolodkin, A.L.; Matthes, D.J.; Goodman, C.S.

Cell 75, 1389-1399, 1993

A;Title: The Semaphorin genes encode a family of transmembrane and secreted growth cone guidance molecules.

A;Reference number: A49423; MUID:94094332; PMID:8269517

A;Accession: B49423

A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-656 <KOL>

A;Cross-references: GB:L26082

C;Genetics:

A;Gene: semaI

A;Cross-references: FlyBase:FBgn0011259

Query Match 16.1%; Score 875; DB 2; Length 656;
Best Local Similarity 35.6%; Pred. No. 1.4e-50;
Matches 208; Conservative 95; Mismatches 193; Indels 88; Gaps 20;

Qy 114 KDECHNFIKVLKKNDDALFVCGTNAFNPSCRNYKMD----TLEPFGDEFSGMARCPYDA 169
:|:| |:|::: : |||||:| | | : || | | | |
Db 1 EDDCQNYIRIMVVPSPGRLFVCGTNSFRPMCNTYIISDSNYTLEA---TKNGQAVCPYDP 57

Qy 170 KHANVALFADGKLYSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYG 229
:| : :: || :|| | | | | :|| | :| :|| | | | : |
Db 58 RHNSTSVLADNELYSGTVADFSGSDPIIYRE-----PLQTEQYDSLNLNAPNFVSSFTQG 112

Qy 230 DYIYFFFREIAVEYNTMGKVVFPRVAQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDS 289
|::| ||||| |||: || :: |||:| | | | :|||:| |||:| |
Db 113 DFVYFFFRETAVEFINCGKAIYSRVARVCKWDKGGPHR-FRNRWTSFLKSRNLNCSIPGDY 171

Qy 290 HFYFNILQAVTDVIR----INGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKE 345
||| :|: :::: : : |:|| ||||| |||: : || | | :||
Db 172 PFYFNEIQSASNLVEGQYGSMSKLIYGVFNTPSNSIPGSAVCAFALQDIADTFEGQFKE 231

Qy 346 QKSPDSTWTPVPDERVPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSI 405
| :| | || : :|| |||| | : | || ||||| |||| ||:
Db 232 QTGINSNWLPVNNAKVPDRPGSC-----HNSRALPDPTLNFIKTHSLMDENVPAP 283

Qy 406 FNRPWFLRTMVRYRLTKIAVD----TAAGPYQNHTVVFLGSEKGIILKFL-ARIGNSGFL 460
|::| :|| || |:||| | | : : |:|:|: | |:| : | :|
Db 284 FSQPILVRTSTIYRFTQIAVDAQIKTPGG--KTYDVI FVGTDHGKIIKSVAESADSADK 341

Qy 461 NDSLFLLEMSVYNSEKCSYDGVEDKRIM-GMQLDRASSSLY-----VAFSTCVIKVPLG 513
|: :||: | : : : |: || | : | : : | : : |
Db 342 VTSVVEEIDVLTKS----EPIRNLEIVRTMQYDQPKDGSYDDGKLIIVTDSQVVAIQLH 397

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Qy      514 RC--ERHGKCKKTCIASRDPYCGWIKGEGAC-SHLSPN--SRLTFEQDIERGNTDGLGDC 568
      ||  ::  | : |:| :||| | | | | || :|  | |::  |
Db      398 RCHNDKITSCSE-CVALQDPYCAWDKIAGKCRSHGAPRWLEENYFYQNVATGQ----- 449

Qy      569 HNSFVALNGHSSSLLPSTTTSDSTAQEGYESRGGMLDWKHLDSPDSTDPLGAVSSSHNHQ 628
      |::      : |: | ||  | |  ||||  |
Db      450 -----HAACPSGKINSKDANAGEGKGFRNDM----DLLDS-----RRQ 483

Qy      629 DKKGVIRESYLKGHD-----QLVPVTLIAIAVILAFVMGAVFS 666
      |  | ::  | :      ::      ::| : |:| |
Db      484 SKDQEIIDNIDKNFEGPQTSADIINAQYTVETLVMAGVLAGSIFS 527

```

RESULT 3

D49423

semaphorin III precursor - human

C;Species: Homo sapiens (man)

C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 24-Sep-1999

C;Accession: D49423

R;Kolodkin, A.L.; Matthes, D.J.; Goodman, C.S.

Cell 75, 1389-1399, 1993

A;Title: The Semaphorin genes encode a family of transmembrane and secreted growth cone guidance molecules.

A;Reference number: A49423; MUID:94094332; PMID:8269517

A;Accession: D49423

A;Status: preliminary; nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-771 <KOL>

A;Cross-references: GB:L26081; NID:g799328; PIDN:AAA65938.1; PID:g436560

C;Genetics:

A;Gene: GDB:SEMA1

A;Cross-references: GDB:283448

C;Superfamily: semaphorin

```

Query Match          15.6%;  Score 852.5;  DB 2;  Length 771;
Best Local Similarity 32.1%;  Pred. No. 5.8e-49;
Matches 208;  Conservative 106;  Mismatches 250;  Indels 83;  Gaps 20;

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Qy      44 HKPGRNTTQRHRLDIQMIMIMNGT-----LYIAARDHIYTV 80
      :: |:|  | :| : ::  |  ||: |:|::|
Db      22 YQNGKNNVPRKLKLSYKEMLESNNVITFNGLANSSSYHTFLLDEERSRLYVGAKDHIFSFD 81

Qy      81 IDTSHTEEIYCSKKLTWKSQRQADVDTCRMKGKH-KDECHNFIKVLKKND DALFVCGTNA 139
      :  |  ::|  | |:  ||  || |||||  |  |: ||| |
Db      82 L-----VNIKDFQKIVWPVSYTRRDECKWAGKDILKECANFIKVLKAYNQTHLYACGTGA 136

Qy      140 FNPSCR-----NYKMDTLEPGDEF--SGMARCPYDAKHANVALFADGKLYSATVTDFLA 192
      |:| |  ::  | :  :  :| : ||| |  :| ||:| | | ||:
Db      137 FHPICTYIEIGHHPEDNIFKLENSHFENGGRGKSPYDPKLLTASLLIDGELYSGTAADFMG 196

Qy      193 IDAVIYRSLGESPTLRVTKHDSKWLEKPYFVQA-----VDYGDYIYFFFREIAVEYNT 245
      |  |:|:|  :|| :||:| | :| |  |  | :||| | |::
Db      197 RDAIFRTLGHHPPIRTEQHD SRWLNDPKFISAHLISESDNPEDDKVYFFFRENAIDGEH 256

Qy      246 MGKVVFP RVAQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPG----DSHFYFNILQAVTD 301
      ||  |: |:| | | |  | | :|:| | | | | | | | | | | | | | | | | | |
Db      257 SGKATHARIGQICKNDFGG-HRSLVNKWTTF LKARLICSVPGPNGIDTHF-----DELQD 310

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Qy	302	VIRINGRD-----VVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVP	357
		: : : : : : :	
Db	311	VFLMNFKDPKNPVVYGVFTTSSNIFKGSAVCMYSMSDVRRVFLGPYAHRDGPYQWVPY-	369
Qy	358	DERVPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVR	417
		: : : : : : : :	
Db	370	QGRVPYPRPGTCP-SKTFGGFDSTKDLPPDVITFARSHPAMYNPVFPMNNRPIVIKTDVN	428
Qy	418	YRLTKIAVDTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLNDSLFEEMSVYNSEKC	477
		: : : : : : : : : : : : : : :	
Db	429	YQFTQIVVDRVDAEDGQYDVMFIGTDVGTVLKVVSI PKETWYDLEEVILLEEMTVFR----	484
Qy	478	SYDGVEDKRIMGMLDRASSSLYVAFSTCVIKVPLGRCERHGKCKKTCIASRDPYCGWIK	537
		: : : : : : : : : : : :	
Db	485	-----EPTAISAMELSTKQQQLYIGSTAGVAQLPLHRCDIYGKACAECCCLARDPYCAW--	537
Qy	538	EGGACSHLSPNS-RLTFEQDIERGNTDGLGDC----HNSFVALNGHS--SSLLPSTTTSD	590
		: : : : : : :	
Db	538	DGSACSRYPFTAKRRTRRQDIRNG--DPLTHCSDLHHDNH---HGHSPEERI IYGVENSS	592
Qy	591	STAQEGYESRGGMLDWKHLSDSPDSTDPLGAVSSSHNHQDKKGVIRE	637
		: : : : : : : : : : : : :	
Db	593	TFLECSPKSORALVYWOFORRNEERKEEI-RVDDHIIRTDQGLLLRS	638


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      :|      | :|||: | || |      : : | | : |||: :| : :: :|:
Db      111 ILYSSEPGKLVICGTNSYKPLCRTYAFKEGKYLVEKEVEGIGLCPYNPEHNSTSVSYNGQ 170

Qy      182 LYSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYFFFREIAV 241
      |:|||| || | :|| | | | | | | | :| ||||:|:| ||
Db      171 LFSATVADFSGGDPLIYRE-----PQRTSLDLKQLNAPNFVNSVAYGDYIFFFYRETAV 225

Qy      242 EYNTMGKVVFPRAQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDSHFYFNILQAVTD 301
      || |||: | |:| |:| || : : : ||||| |||: |||: :|: :|
Db      226 EYMNCGKVIYSRVARVCKDDKGGPHQSRDR-WTSFLKARLNCSIPGEYPFYFDEIQSTSD 284

Qy      302 VI--RINGRD--VVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVP 357
      :: | | | : : | :| | | :|| | | | | | | : : | | | |
Db      285 IVEGRYNSDDSKIIYGILTPVNAIGGSAICAYQMADILRVFEGSFKHQETINSNWLVPV 344

Qy      358 DERVPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVR 417
      ||:|||| | | : | | :|||| | |: | |:| :| :| : :
Db      345 QNLVPEPRPGQCVRDSRI-----LPDKNVNFIKTHSLMED-VPALFGKPVLRVSLQ 395

Qy      418 YRLTKIAVDTAAGPYQNH--TVVFLGSEKGIILKFLARIGNSGFLNDSLFLLEMSVYNSE 475
      || | | | | | | | :|:|:| :| :|
Db      396 YRFTAITVDPQVKTINNQYLDVLYIGTDDGKVLK----- 429

Qy      476 KCSYDGVEDKRIMGMQLDRASSSLYVAFSTCV-----IKVP----- 511
      : : | : || : | | :|:
Db      430 -----AVNIPKRHAKALLYRKYRTSVHPHGAPVKQLKIAPGYGKVVVVGKDEIR 478

Qy      512 ---LGR CERH GKCKKTCIASRDPYCGWIKEGGACSHLSPNSRLTF-EQDIERN----- 561
      | | :| | | :|:| | : | : | | :|:
Db      479 LANLNHCASKTRC-KDCVELQDPHCAWDAKQNLCSIDTVTSYRFLIQDVVRGDDNKCWS 537

Qy      562 --TDGLGDCHNSFVALNGHSSSLPSTTTSDSTAQEGYESRGGMLDWKHLLDSPDSTDPL 619
      || | | | | | | :| :| :| :| :| :|
Db      538 PQTDKKTVIKNK-----PSEVENEIT-----NSIDEKDL---DSSDPL 572

Qy      620 GAVSSHNHQDKKGVIRESYLKG---HDQLVPVT--LLAIAVILAFVMGA---VFSGITVY 671
      : | | | : : | || | | | : : :| :| :| :| :|
Db      573 IKTGLDDSDCDPV-SENSIGGCAVRQQLVIYTAGTLHIVVVVVSIVGLFSWLYSGLSVF 631

Qy      672 CV--CDHRRKDVAVVQRKE--KELTHSRRGSMS-SVTKLSGLFGDTQSKDPKPEAILTPL 726
      | : : : : : | : : | : | | | | :| :| :
Db      632 AKFHSDSQYPEAPFIEQHNHLERLSANQTGYLTFRANKAVNLVVKVSSSTPRPKKDNLDV 691

Qy      727 MHNGKLATPGNTAKM 741
      : :|: | | :
Db      692 SKDLNIASDGTLQKI 706

```

RESULT 5

I48747

semaphorin D - mouse

C;Species: Mus musculus (house mouse)

C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 24-Sep-1999

C;Accession: I48747

R;Puschel, A.W.; Adams, R.H.; Betz, H.

Neuron 14, 941-948, 1995

A;Title: Murine semaphorin D/collapsin is a member of a diverse gene family and creates domains inhibitory for axonal extension.
A;Reference number: I48744; MUID:95267431; PMID:7748561
A;Accession: I48747
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-772 <RES>
A;Cross-references: EMBL:X85993; NID:g854329; PIDN:CAA59985.1; PID:g854330
C;Genetics:
A;Gene: semD
C;Superfamily: semaphorin

Query Match 15.5%; Score 842.5; DB 2; Length 772;
Best Local Similarity 34.3%; Pred. No. 2.7e-48;
Matches 200; Conservative 85; Mismatches 225; Indels 73; Gaps 16;

```

Qy      47 GRNTTQRHRLDIQMIMMNGT-----LYIAARDHIYTVDIDT 83
      |:| | | :| : :: | | | :| | | :| : ::
Db      25 GKNNVPRCLKLSYKEMLESNNVITFENGLANSSSYHTFLLDEERSRLYVGAKDHIFSFLN-- 82

Qy      84 SHTEEIYCSKKLTWKSQRQADVDTCRMKGKH-KDECHNFIKVLLKKNDDALFVCGTNAFNP 142
      | :| :| | | | :| | | | | | | | | | | :| | | | | :|
Db      83 ---VNIKDFQKIVWPVSYTRRDECKWAGKDILKECANFIKVLEAYNQTHLYACGTGAFHP 139

Qy     143 SCR-----NYKMDTLEPFGDEF--SGMARCPYDAKHANVALFADGKLYSATVTDFLAIDA 195
      | :| :| :| :| :| :| | | | :| | | | | | | | :| |
Db     140 ICTYIEVGHHPEDNIFKLQDSHFENGRGKSPYDPKLLTASLLIDGELYSGTAADFMRGRDF 199

Qy     196 VIYRSLGESPTLRTVKHDSKWLKEPYFVQA-----VDYGDYIYFFFREIAVEYNTMGK 248
      | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db     200 AIFRTLGDHHPIRTEQHDSRWLNDPRFISAHLIPESDNPEDDKVYFFFRENAIGGEHSGK 259

Qy     249 VVFPRVAQVCKNDMGGSQRVLEKQWTSFLKARLNCVPG----DSHFYFNILQAVTDVIR 304
      | :| :| | | | | | | | :| :| :| | | | | | | | :| :|
Db     260 ATHARIGQICKNDFGG-HRSLVNKWTTFCLKARLICSVPGPNGIDTHF-----DELQDVFL 313

Qy     305 INGRD----VVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVPDER 360
      :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db     314 MNSKDPKNPIVYGVFTTSSNIFKGSAVCMYSMSDVRVFLGPYAHRDGPNYQWVPY-QGR 372

Qy     361 VPKPRPGCCAGSSSLERYATSNEFPDDLNFIFKTHPLMDEAVPSIFNRPWFLRTMVRYRL 420
      | | | | | | | :| :| :| :| :| :| :| :| :| :| :| :|
Db     373 VPYPRPGTCP-SKTFGGFDSTKDLRDDVITFGRSHPAMYNPVFPINNRPIMIKTDVNYQF 431

Qy     421 TKIAVDTAAGPYQNHTVVFGLGSEKGIILKFLARIGNSGFLNDSLFLEEMSVYNSEKCSYD 480
      | :| | | :| :| :| :| :| :| :| :| :| :| :| :| :|
Db     432 TQIVVDRVDAEDGQYDVMFIGTVDGTVLKVVSVPKETWHDLEEVLLLEEMTVFR----- 484

Qy     481 GVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRRCERHGKCKKTCIASRDPYCGWKEGG 540
      | | | | | :| :| :| :| :| :| :| :| :| :| :| :|
Db     485 --EPTTISAMELSTKQQQLYIGSTAGVAQLPLHRCDIYGKACAECLARDPYCAW--DGS 540

Qy     541 ACSHLSPNS-RLTFEQDIERGNTDGLGDCHNSFVALNGHSSSL 582
      :| | | :| | | | | | | :| :| :| :| :| :|
Db     541 SCSRYFPTAKRRTRRQDIRNG--DPLTHCSDLEDHDNHHGPSL 581

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RESULT 6
 A49069
 collapsin - chicken
 C;Species: Gallus gallus (chicken)
 C;Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 24-Sep-1999
 C;Accession: A49069
 R;Luo, Y.; Raible, D.; Raper, J.A.
 Cell 75, 217-227, 1993
 A;Title: Collapsin: a protein in brain that induces the collapse and paralysis
 of neuronal growth cones.
 A;Reference number: A49069; MUID:94006554; PMID:8402908
 A;Accession: A49069
 A;Status: preliminary; not compared with conceptual translation
 A;Molecule type: mRNA
 A;Residues: 1-772 <LUO>
 A;Cross-references: GB:U02528; NID:g410078; PIDN:AAC59638.1; PID:g410079
 C;Superfamily: semaphorin

Query Match 15.4%; Score 839.5; DB 2; Length 772;
 Best Local Similarity 35.2%; Pred. No. 4.3e-48;
 Matches 198; Conservative 87; Mismatches 220; Indels 57; Gaps 17;

Qy	68	LYIAARDHIYTVDIDTSHTEEIYCSKKLTWKSQRQADVDTCRMKGKH-KDECHNFIKVLK	126
		: : : : : : : :	
Db	69	LYVGAKDHIFSFL-----VNIKEYQKIVWPVSHSRDECKWAGKDILRECANFIKVLKT	123
Qy	127	KNDDALFVCGTNAFNPSCR-----NYKMDTLEPFGDEF--SGMARCPYDAKHANVALFAD	179
		: : : : : : :	
Db	124	YNQTHLYACGTGAFFHPMCTYIEVGSHPEDNIFRMEDSHFENGGRGKSPYDPKLLTASLLVD	183
Qy	180	GKLYSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQA-----VDYGDYI	232
		: : : : : : : : : :	
Db	184	GELYSGTAADFMRDFAIFRTLGHHPHPIRTEQHDSRWLNDRPFISAHLPESDNPEDDKI	243
Qy	233	YFFFREIAVEYNTMGKVVFPRVAQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPG----D	288
		: : : : : : : :	
Db	244	YFFFRENAIDGEHTGKATHARIGQICKNDFGG-HRSLVNKWTTFLLKARLICSVPGPNGID	302
Qy	289	SHFYFNILQAVTDVIRINGRD-----VVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFK	344
		: : : : : : : : :	
Db	303	THF-----DELQDVFLMNSKDPKNPIVYGVFTTSSNIFKGSAVCMYSMTDVRVFLGPYA	357
Qy	345	EQKSPDSTWTPVPDERVPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPS	404
		: : : : : : : : :	
Db	358	HRDGPNYQWVPY-QGRVPYPRPGTCP-SKTFGGFDSTKDLPEDEVITFARSHPAMYNPVFP	415
Qy	405	IFNRPWFLRTMVRYRLTKIAVDTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLNDSL	464
		: : : : : : : : : : : : :	
Db	416	INSRPIMIKTDVDYQFTQIVVDRVDAEDGQYDVMFIGTDIGTVLKVVSIPKETWHELEEV	475
Qy	465	FLEEMSVYNSEKCSYDGVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRGERHGKCKKT	524
		: : : : : : : : : :	
Db	476	LLEEMTVFR-----EPTVISAMKISTKQQQLYIGSATGVSQPLPHRCDVYGKACAE	526
Qy	525	CIASRPYCGWIKEGGACSHLSPNS-RLTFEQDIERGNTDGLGDCHNSFVALNGHSSSLL	583
		: : : : : : : : : :	
Db	527	CCLARDPYCAW--DGSSCSRYFPTAKRRTRRQDIRNG--DPLTHCSD---LQHHDN---	575

Qy 584 PSTTTSDSTAQEGYESRGGMLD 605
 || | : | | : | :
 Db 576 PSGQTLEEKIIYGVENSSTFLE 597

RESULT 7

JC5928

semaphorin F precursor - human

C;Species: Homo sapiens (man)

C;Date: 10-Apr-1998 #sequence_revision 08-May-1998 #text_change 17-Nov-2000

C;Accession: JC5928

R;Simmons, A.D.; Pueschel, A.W.; McPherson, J.D.; Overhauser, J.; Lovett, M.
 Biochem. Biophys. Res. Commun. 242, 685-691, 1998

A;Title: Molecular cloning and mapping of human semaphorin F from the Cri-du-
 chat candidate interval.

A;Reference number: JC5928; MUID:98125554; PMID:9464278

A;Accession: JC5928

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-1074 <SIM>

A;Cross-references: GB:U52840; NID:g2772583; PIDN:AAC09473.1; PID:g2772584

A;Experimental source: brain

C;Comment: This protein disrupts normal brain development and leads to some of
 the features of Cri-du-chat.

C;Genetics:

A;Gene: semaF

C;Superfamily: human semaphorin F; thrombospondin type 1 repeat homology

F;1-20/Domain: signal sequence #status predicted <SIG>

F;50-533/Domain: semaphorin #status predicted <SEM>

F;840-896/Domain: thrombospondin type 1 repeat homology <THR3>

F;971-993/Domain: transmembrane #status predicted <TMM>

Query Match 15.2%; Score 830; DB 2; Length 1074;
 Best Local Similarity 36.2%; Pred. No. 3.1e-47;
 Matches 199; Conservative 90; Mismatches 211; Indels 50; Gaps 17;

Qy 68 LYIAARDHIYTVDIDTSHTEEIYCSKKLTWKSQRQADVDCRMKGKHKDECHNFIKVLLKK 127
 | : ||::: : : |:: : : | : :| | || |::|| |::|||
 Db 70 LVVGARNYLFRLQL-----EDLSLIQAVEWECDEATKKACYSKGSKEECQNYIRVLL-V 123

Qy 128 NDDALFVCGTNAFNPSCRNYKMDTLEPFGDEFSGMARCPYDAKHANVALF-ADGKLYSAT 186
 | || ||||| | | | : | | : ||||| | : : || | |::|||
 Db 124 GGDRLFTCGTNAFTPVCTNRSLSNLAEIHDQISGMARCPYSPQHNSTALLTAGGELYAAT 183

Qy 187 VTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYFFFREIAVEYNTM 246
 || | | ||||| | ||| ::||| | | | : | |:: ||||| ||:::
 Db 184 AMDFPGRDPAIYRSLGILPPLRTAQYNSKWLNEPNFVSSYDIGNFTYFFFRENAVEHD-C 242

Qy 247 GKVVFPRAQVCKNDMGGSQRVLEKQWTSFLKARLNCSPVGD SHFYFNILQAVTDVIRIN 306
 || || | |::|||::|| : :|| ||::|:||||| ||: ||:| ||: : :
 Db 243 GKTVFSRAARVCKNDIGG-RFLEDTWTTFMKARLNC SRPGEVPFYYNELQSTFFLPPEL- 300

Qy 307 GRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVPDERVPKPRP 366
 |:: |:: ||| |||| :: | | |:: | | | | : | |
 Db 301 --DLIYGIFTTNVNSIAASAVCVFNLSAIAQAFSGPFPKYQENSRSALWLPYPN---PNPHF 355

```

Qy      367 GCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRLTKIAVD 426
      |      |      |      |      ||      |      |      |      |      |      |      |
Db      356 QCGTVDQGLYVNLTERNL-QDAQKFILVH----EVVQPVTTPVPSFMEDNSRF--SHVAVD 408

Qy      427 TAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLNDSLFLEEMSVYNSEKCSYDGVEDKR 486
      |      ::| ::| ||      :      :      :      |      ||| ::      :      :
Db      409 VVQGREALVHIIYLATDYGTIKKVRVPLNQT---SSSCLLEEIELEFPERR-----REP 458

Qy      487 IMGMLDRASSSLYVAFSTCVIKVPLGR CERH GKCKKTCIASRDPYCGWIKEGGACSHLS 546
      |      ::| :| |||      |::|| ||: : : : ||| ::||| ||      | :|
Db      459 IRSLQILHSQSVLFVGLREHVVKIPLKRCQFY-RTRSTCIGAQDPYCGWDVVMKKCTSLE 517

Qy      547 PNSRLT-FEQDIERGNTDGLGDCHNSFVALNGHSSSLLPST--TTSDSTAQEGYESRGGM 603
      :      :| :|| |      |      : :||      |      | :| :|      |
Db      518 ESLSMTQWEQSISA-----CPTRNLTVDGHFGVWSPWTPCTHTDGS AV-----GSC 563

Qy      604 LDWKHLLDSP 613
      |      |||
Db      564 LCRTRSCDSP 573

```

RESULT 8

G01856

semaphorin V - human

C;Species: Homo sapiens (man)

C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 24-Sep-1999

C;Accession: G01856

R;Sekido, Y.

submitted to the EMBL Data Library, June 1995

A;Reference number: G08634

A;Accession: G01856

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-749 <SEK>

A;Cross-references: EMBL:U28369; NID:g974283; PIDN:AAD09138.1; PID:g974284

C;Superfamily: semaphorin

```

Query Match          15.2%; Score 826; DB 2; Length 749;
Best Local Similarity 34.7%; Pred. No. 3.3e-47;
Matches 198; Conservative 88; Mismatches 228; Indels 56; Gaps 16;

```

```

Qy      66 GTLYIAARDHIYTVDIDTSHTEEIYCSKKLTWKS RQADVDTCRMKGKH-KDECHNFIKVL 124
      | ||: | :|: ::::|      :|| | :      :|      ||      || ||:|:|
Db      65 GRLFVGAENHVASLNLDNISK R---AKKLAWPAPVEWREECNWAGKDIGTECMNFVKLL 120

Qy      125 LKKND DALFVCGTNAFNPSCRNYKMD-----TLEPF GDEFSGMARCPYDAKHANVAL 176
      |      | ||| ||:|:|      :      :| |      | : ||| :|      :
Db      121 HAYNRTHLLACGTGA FHPTCAFVEVGHRAEEPVLRLDP-GRIEDGKGKSPYDPRHRAASV 179

Qy      177 FADGKLYSATVTD FLAIDAVIYRSLGESPTLR TVKHDSKWLKEPYFVQAV-----DYG 229
      :|||      | :      | :|||: | :|||      ||:| || |||
Db      180 LVGEELYSGVAADLMGRDFTIFRSLGQRPSLRTEPHDSRWLNPKFVKVFWIPESENPDD 239

Qy      230 DYIYFFFREIAVE-YNTMGKVVFPRVAQVCKNDMGGSQRVLEKQWTSFLKARLNCSVP-- 286
      | ||||| |||      :::      || |::|:| || |      :||:||||| |||
Db      240 DKYIYFFRETAVEAAPALGRLSVSRVGQICRNDVGG-QRSLVNKWTTF LKARLVCSVPGV 298

```

```

Qy      287 -GDSHFYFNILQAVTDVIRINGRD----VVLATFSTPYNSIPGSAVCAYDMLDIASVFTG 341
      ||:||      : ||  :: ||      :: | ||| :  |||| | | :  | |
Db      299 EGDTHF-----DQLQDVFLLSRDHRTPLLYAVFSTSSSIFQGSAVCVYSMNDVRRFLG 353

Qy      342 RFKEQKSPDSTWTPVNDERVPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEA 401
      |  :: |  |      ||| |||| |  | :  :::: :||| :  | : ||| :
Db      354 PFAHKEGPMHQWVSY-QGRVPYPRPGMCP-SKTFGTFSSTKDFPDDVIQFARNHPLMYS 411

Qy      402 VPSIFNRPWFLRTMVRYRLTKIAVDTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLN 461
      |      || ||:  | |:|| |  |  :: |:||:: | :|| ::  |
Db      412 VLPTGGRPLFLQVGANYTFTQIAADRVAAADGHYDVLFIGTDVGTVLKVISVPKGSRPSA 471

Qy      462 DSLFLEEMSVYNSEKCSYDGVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRRCERHGKC 521
      : | |||: |:      :  : ||:  ||| : | :: | | ||:
Db      472 EGLLLEELHVFE-----DSAAVTSMQISSKRHQLYVASRSAVAQIALHRCAAHGRV 522

Qy      522 KKTCIASRDPYCGWIKEGGACSHLSPNSRLTF-EQDIERGNTDGLGDCHNSFVALNGH-- 578
      |  :||| |  :| ||:  |::: | ||: |  |  :| || |
Db      523 CTECCLARDPYCAW--DGVACTRFQPSAKRRFRQDVRNGDPSTLCSGDSSRPALLEHKV 580

Qy      579 -----SSSLPSTTTSDSTAQEGYESRGGM 603
      ||: |  |  |  |  ||:
Db      581 FGVEGSSAFLECEPRSLQARVEWTFQRAGV 610

```

RESULT 9

I48744

semaphorin A - mouse

C;Species: Mus musculus (house mouse)

C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 24-Sep-1999

C;Accession: I48744

R;Puschel, A.W.; Adams, R.H.; Betz, H.

Neuron 14, 941-948, 1995

A;Title: Murine semaphorin D/collapsin is a member of a diverse gene family and creates domains inhibitory for axonal extension.

A;Reference number: I48744; MUID:95267431; PMID:7748561

A;Accession: I48744

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-748 <RES>

A;Cross-references: EMBL:X85990; NID:g854323; PIDN:CAA59982.1; PID:g854324

C;Genetics:

A;Gene: semA

C;Superfamily: semaphorin

Query Match 14.7%; Score 803; DB 2; Length 748;

Best Local Similarity 35.5%; Pred. No. 1.1e-45;

Matches 191; Conservative 80; Mismatches 205; Indels 62; Gaps 18;

```

Qy      66 GTLYIAARDHIYTVDIDTSHTEEIYCSKKLTWKSQRQADVDCRMKGKH-KDECHNFIKVL 124
      | |:: | ::: :: :|      :|| | :  : |  ||  || ||:::|
Db      65 GRLFVGAENHVASLSLDNISKR----AKKLAWPAPVEWREECNWAGKDIGTECMNFVRL 120

Qy      125 LKKND DALFVCGTNAFNPSCRNYKMDTL-----EPFGDEFSGMARCPYDAKHANVA 175
      |  |  | | ||:|:|  :: |  |  |  |  : ||| :|  :
Db      121 HAYNHTLLACRTGAFHPTCALWRWATAGGTHASTGPEKLED---GKGKTPYDPRHRPPS 177

```

Qy 176 LFADGKLYSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAV-----DY 228
 : :||| | : | |:||||:|:||| ||:| | ||:
 Db 178 VLVGEELYSGVTADLMGRDFTIFRSLGQNPSLRTEPHDSRWLNPEKFKVFWIPESENP 237

Qy 229 GDYIYFFFREIAVE-YNTMGKVVFPRVAQVCKNDMGGSQRVLEKQWTSFLKARLNCSVP- 286
 | ||||| | | | | :| | |:|:|:| | | | :|:| | | | | | | |
 Db 238 DDKIYFFFRESAVEAAPAMGRMSVSRVGQICRNDLGG-QRSLVNKWTTFKARLVCSVPG 296

Qy 287 --GDSHFYFNILQAVTDVIRINGRD----VVLATFSTPYNSIPGSAVCAYDMLDIASVFT 340
 ||:| | : | | : | | : | | | | | | | | : | |
 Db 297 VEGDTHF-----DQLQDVFLSSRDRQTPLLYAVFSTSSGVFQGSAVCVYSMNDVRR AFL 351

Qy 341 GRFKEQKSPDSTWTPVPDERVFKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDE 400
 | : : | | | | | | | | : : : : : | | : | | | |
 Db 352 GPLPHKEGPTHQWVSY-QGRVPYPRPGMCP-SKTFGTFSSTKDFPDDVIQFGRNHPLMYN 409

Qy 401 AVPSIFNRPWFLRTMVRYRLTKIAVDTAAGPYQNHTVVFLGSEKGIILKFLA----RIGN 456
 | : ||||: | |:| | | : | |:|:|:| | :|| : : | |
 Db 410 PVLPMGGRPLFLQVGAGYTFTQIAADRVAAADGHYDVLFIGTDVGTVLKVISVPKGRPN 469

Qy 457 SGFLNDSLFLLEEMSVYNSEKCSYDGVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRCE 516
 | : | |||: | : | | | : | | | | | | | : : | | |
 Db 470 S-----EGLLLEELQVFE-----DSAAITSMQISSKRQQLYVASRAVAQIALHRCT 516

Qy 517 RHGKCKKTCIASRDPYCGWIKEGGACSHLSPNSRLTF-EQDIERGNTDGL--GDCHNS 571
 | : | :| | | | | :| | | : | : | | | | : | | | : |
 Db 517 ALGRACAECCLARDPYCAW--DGSACTRFQPTAKRRFRRQDIRNGDPSTLCSGDSSH 572

RESULT 10

I58169

semaphorin III - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 24-Sep-1999

C;Accession: I58169

R;Messersmith, E.K.; Leonardo, E.D.; Shatz, C.J.; Tessier-Lavigne, M.; Goodman, C.S.; Kolodkin, A.L.

Neuron 14, 949-959, 1995

A;Title: Semaphorin III can function as a selective chemorepellent to pattern sensory projections in the spinal cord.

A;Reference number: I58169; MUID:95267432; PMID:7748562

A;Accession: I58169

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-666 <RES>

A;Cross-references: GB:L40484; NID:g703189; PIDN:AAA73934.1; PID:g703190

C;Genetics:

A;Gene: SemaIII

C;Superfamily: semaphorin

Query Match 14.6%; Score 793.5; DB 2; Length 666;
 Best Local Similarity 34.1%; Pred. No. 4.1e-45;
 Matches 188; Conservative 89; Mismatches 226; Indels 49; Gaps 15;

Qy 116 ECHNFIKVLLKKNDDALFVCGTNAFNPSR-----NYKMDTLEPFGDEF--SGMARCPYD 168
 || ||||| | | |: ||| |:| | : : | : | : | : |||
 Db 7 ECANFIKVLEAYNQTHLYACGTGAFHPICTYIEVGHPEDNIFKLQDSHFENGGRGKSPYD 66

A; Introns: 36/1; 70/2; 85/3; 194/2; 221/1; 253/3; 301/1; 352/3; 522/2; 560/1; 599/3; 655/3

Query Match 14.5%; Score 789; DB 2; Length 712;
Best Local Similarity 28.7%; Pred. No. 9.1e-45;
Matches 229; Conservative 129; Mismatches 282; Indels 158; Gaps 29;

```
Qy      6 LLLYFTLLHFAGAGFPEDSEPISISHGNYTKQYP-----VFVGHKPGRNNTQQRHRLDIQ 59
      ||| | ::          || | : |          | : | : | |          |
Db      7 LLLLFNVV-----RSSEAIT---GGVVNLRPKQIINSVGIGDRFGGIGTSSDESDFH 55

Qy     60 MIMIMNG-TLYIAARDHIYTVDIDTSHTEEIYCSKKLTWKSQRQADVDTCRMKGKHKDECH 118
      :: :| :| : ||: :| : : |          : : | : ||          :: | |||| | :|
Db     56 KLLAADGDSLLVGARNAVYNLSLST-----LSVNHKIDWKPPAEHIEECIMKGKSKTDCQ 110

Qy    119 NFIKVLKKND DALFVCGTNAFNPSCRNYKMDTLEPGF----DEFSGMARCPYDAKHANV 174
      | :| :| | :|          |||| :| :| | || |          | : ||          :| |          ||| || :
Db    111 NYIRVLARKSAGVSLVCGTHAFSPKCREY---TVTEFGIRNTRQFDGQGISPYDPKHNS 167

Qy    175 ALFADG--KLYSATVTDFLAIDAVIYR-SLGESPT-----LRTVKHDSKWLKEPYFVQA 225
      ||: | :| : ||||| : ||: ||| :: | :| :          :|| :| :| : | | ||
Db    168 ALYVPGTNQLFVATVTDFVGN DALIYRKTIDETPSSKSAANIRTQSYDARVLNAPNFVAT 227

Qy    226 VDYGDYIYFFFREIAVEY--NTMGKVVFPRVAQVCKNDMGGSQRVLEKQWTSFLKARLNC 283
      | ::| :| :| |||| | |          : : ||| :| |||| ||: |          : :| :| :| |||||
Db    228 FAYKEHVYFWFREIASEAIDNNEEPQIYARVARVCKNDKGGA-RPANERWTSYLKARLNC 286

Qy    284 SVP-GDSHFYFNILQAVTDVIRI-NGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVF-T 340
      | :| | | |||| | :| :| | |          ||          |||| : : |||| : | | | |
Db    287 SLPSGSSPFYFNELKAVSDPIDAGNNNHVVYTVFSTPDS DVRMSAVCKFMSKKIREEDFN 346

Qy    341 GRFKEQKSPDSTWTPVPDERVPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDE 400
      | || | : | |          ||||| | : | :          : | :| :| :| ||| :
Db    347 GTFKHQNNAQSMWMAFNREVPKPRPGSCSPDST-----KLPENTVSFILHHPPLLHR 398

Qy    401 AVPSIFNRPWFLRTMVRYRLTKIAV---DTAAGPYQNHTVVFLGSEKGIILKFLARIGNS 457
      :||: | : |          ||:| |          | | : | : :| :| : | :|| : ||:
Db    399 PIPSV-AAPLLVEGADRADLTQITVLPVRVAVGGH-NYDILFIGTSDGKVLKVVEVDGNA 456

Qy    458 GFLND-SLFLEEMSVYNSEKCSYDGVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRCE 516
      : :| : : |          |          | : : : : :| : |
Db    457 TVIQSATVFQRGVPIVN-----LLTTKESVVIVSADEIASLPVHNCA 498

Qy    517 RHGKCKKTCIASRDPYCGWIKGACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALN 576
      : | | | : :| :| |          | |          : | :| :| :| : | :
Db    499 QQTSCSK-CVQLQDPHCAWDSSIARCVHGGSWTGDQFIQNMVFGQSE---QCPEGIIV-- 552

Qy    577 GHSSSLLPSTTTSDSTAQEGYESRGGMLDWKHL LDPDSTDPLGAVSSHNH QDKKGVIRE 636
      : : | :|          |||          |
Db    553 -----REVFDNESEAQPEAVS-----RS 571

Qy    637 SYLKGH DQLVPVTL LAIVILAFVMGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHS-- 694
      | | | : | : | :| :| :| :| | || |          :| : | : |
Db    572 GYPKEHSTITVVLVAASLISLIIGA-FIGIRV-----NRWAATSEPHRSASSTSGSDY 625

Qy    695 -----RRGSMSSVTKLSGLFGDTQSKDPKPEAILTPLMHNGKLATPGNTAKMLIKA 745
      | | :| :| :|          |          : | : : | | |
```

Db 626 DSFGRARLTRHDSLTTATKVDHGF-----VPQSKQSVDATSLVMSINA 668
 Qy 746 DQHHLDLTALPTPESTPT 763
 | : :: : :||:
 Db 669 THHPMSMSQHSGSINTPS 686

RESULT 12

C49423

semaphorin II precursor - fruit fly (*Drosophila melanogaster*)

C;Species: *Drosophila melanogaster*

C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 07-May-1999

C;Accession: C49423

R;Kolodkin, A.L.; Matthes, D.J.; Goodman, C.S.

Cell 75, 1389-1399, 1993

A;Title: The Semaphorin genes encode a family of transmembrane and secreted growth cone guidance molecules.

A;Reference number: A49423; MUID:94094332; PMID:8269517

A;Accession: C49423

A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-724 <KOL>

A;Cross-references: GB:L26083

C;Genetics:

A;Gene: sema II

A;Cross-references: FlyBase:FBgn0011260

C;Superfamily: semaphorin

Query Match 14.3%; Score 779.5; DB 2; Length 724;
 Best Local Similarity 33.5%; Pred. No. 4.1e-44;
 Matches 193; Conservative 99; Mismatches 199; Indels 85; Gaps 22;

Qy 33 NYTKQYPVFVGHKPGRNTTQRHRLD-----IQMIMIMN---GTLYIAARDHIYTV 79
 | : : | | : | | : | | | | | : | | : : |
 Db 32 NFYYERPCCTGNDQGNNNYGKHGADHVREFNCGKLYYRTFHMNEDRDTLYVGAMDRVFRV 91
 Qy 80 DIDTSHTEEIYCSK-KLTWKSQRQADVDTCRMKGKHK-DECHNFIKVLLKKND-DALFVCG 136
 :: : |:: : : : || : | ||| : : | | ::| : | |::|
 Db 92 NLQNISSN--CNRDAINLEPTRDDVSCVSKGKSQIFDCKNHVRVIQSMQDQDRLYVCG 149
 Qy 137 TNAFNPSCRNY-----KMDTLEPFGDEFSGMARCPYDAKHANVALFADG----- 180
 ||| || :| : : : | | :|:| | | : |:: :
 Db 150 TNAHNP--KDYVIYANLTHLPRSEYVIGVG---LGIACPYDPLDNSTAIYVENGNPGGL 204
 Qy 181 -KLYSATVTDFLAIDAVIYRS-----LGESPTLRTVKHDSKWLKEPYFVQAVDYG DY 231
 ||| | :| | ||:| : | ||:|:| | | : | | : | | :|
 Db 205 PGLYSGTNAEFTKADTVIFRTDLYNTSAKRLEYKFKRTLKYDSKWLDKPNFVGSFDIGEY 264
 Qy 232 IYFFFREIAVEYNTMGKVVFPRVAQVCKNDMGGSQRVLEKQWTSFLKARLNCSPVGD SHF 291
 :| | | | | | | | | | : | :|:| | | :| : | :| | | | | :| :|
 Db 265 VYFFFRETAVEYINC KAVYSRIARVCKKDVGK-KNLLAHNWATY LKARLNC SISGEFPF 323
 Qy 292 YFNILQAVTDVIRINGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDS 351
 ||| :|:| : | | | :| | : | | | : : : | : | | :| | | :|
 Db 324 YFNEIQSVYQLPSDKSR--FFATFTTSTNGLIGSAVCSFHINEIQAAFNGKFKEQSSSNS 381

Qy 352 TWTPVPDERVPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRP-W 410
 | | : | | : | | | | : | | | | : | | : | | :
 Db 382 AWLPVLNSRVPEPRPGTCVNDTS-----NLPDTVLNFIRSHPLMDKAVNHEHNNPVY 433

Qy 411 FLRTMVRYRLT--KIAVDTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLNDSLFLEE 468
 : | : | : | | : | : | : | | : | : | : | : |
 Db 434 YKRDLVFTKLVDKIRIDIL---NQEYIVYVGTNLGRIYKIVQYYRNGESLSKLLDIFE 490

Qy 469 MSVYNSEKCSYDGVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRC-ERHGKCKKTCIA 527
 :: : : | | : : | | : : | | : : | | : : | :
 Db 491 VA-----PNEAIQVMEISQTRKSLYIGTDHRIKQIDLAMCNRRYDNCFR-CV- 536

Qy 528 SRDPYCGWIKEGGACSHLSPNSRLTFEQDIERGNTD 563
 | | | | | | | | | | | | | | | | | | : | : |
 Db 537 -RDPYCGWDKEANTCRPY----ELDLLQDVANETSD 567

RESULT 13

G02173

semaphorin III family homolog - human

C;Species: Homo sapiens (man)

C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 24-Sep-1999

C;Accession: G02173

R;Naylor, S.

submitted to the EMBL Data Library, October 1995

A;Reference number: G09275

A;Accession: G02173

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-753 <NAY>

A;Cross-references: EMBL:U38276; NID:g1061350; PIDN:AAB18276.1; PID:g1061351

C;Superfamily: semaphorin

Query Match 14.1%; Score 768; DB 2; Length 753;
 Best Local Similarity 31.6%; Pred. No. 2.5e-43;
 Matches 191; Conservative 109; Mismatches 207; Indels 98; Gaps 22;

Qy 6 LLLYFTLLHFAGAGFPEDSEPISSHGNKYKQYPVFVGHKPGRNTTQRHRLDIQMI---- 61
 | | : | | | | | | | | | | : :
 Db 6 LLLWASLLTGAWPSFPTQD-----HLP---ATPRVRLSFKELKATG 43

Qy 62 -----MIMNGT-----LYIAARDHIYTVDIDTSHTEEIYCSKKLTWKSQA 102
 : : | | : : : : : : : : : : : : : : : :
 Db 44 TAHFFNFLLNTTDYRILLKDEDHDMYVGSKDYLVDLHDINREPLI----IHWAASPQ 99

Qy 103 DVDTCRMKGKH-KDECHNFIKVLKKNDDALFVCGTNAFNPS-----RNYKMDTL 152
 : : | : | | | | : : : : | : | | | : : | : : | :
 Db 100 RIEECVLSGKDVNGECGNFVRLIQPNRTHLYVCGTGAYNPMCTYVNRGRRAQDY-IFYL 158

Qy 153 EPGDEFSGMARCPYDAKHANVALFADGKLYSATVTDFLAIDAVIYRSLGESPTLRVTKH 212
 | | | | : | | | : : : : | : | | : | : | : : : :
 Db 159 EPERLE-SGKGKCPYDPKLDTASALINEELYAGVYIDFMGTDAAFRTLKGQTAMRTDQY 217

Qy 213 DSKWLKEPYFVQA-----VDYGDYIYFFFREIAVEYNTMGKVVFPRVAQVCKNDMGGSQ 266
 : : | : | : | : | : | : | : | : | : | : | : | : | :
 Db 218 NSRWLNDPFSFIHAELIPDSAENDDKLYFFFRERSAE-APQSPAVYARIGRICLNDDGGHC 276

Qy 267 RVLEKQWTSFLKARLNCSVPGDS--HFYFNILQAV----TDVIRINGRDVVLATFSTPYN 320
 :: | |::| | | | | | | | | | : : | : | | : | : | : :
 Db 277 CLVNK-WSTFLKARLVCSVPGEDGIETHFDELQDVFVQQTQDVR---NPVIYAVFTSSGS 332
 Qy 321 SIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVPDERVPKPRPGCCAGSSSLERYAT 380
 | | | | | | | | | | | | : : | : | | : : | | | | | : :
 Db 333 VFRGSAVCVYSMADIRMVFNPGFAHKEGPNYQWMPF-SGKMPYPRPGTCPGGTFTPSMKS 391
 Qy 381 SNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRLTKIA--VDTAAGPYQNHTV 437
 : : | | : : | | : : | | : | : | | | | | | | | : | :
 Db 392 TKDYPDEVINFMRSHPLMYQAVYPLQRRPLVVRTGAPYRLTTIAVDQVDSADGRYE---V 448
 Qy 438 VFLGSEKGIILKFLARIGNSGFLNDSLFLEEMSVYNSEKCSYDGVEDKRIMGMQLDRASS 497
 : | | : : | : | : : : | | | : | : : : | :
 Db 449 LFLGTDGRGTQKVIV-LPKDDQEMEELMLEEVEVFK-----DPAPVKMTTISSKRQ 498
 Qy 498 SLYVAFSTCVIKVPLGRGERHGKCKKTCIASRDPYCGWIKEGGACSHLSPNS-RLTFEQD 556
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 Db 499 QLYVASAVGVTHLSLHRCQAYGAACADCCCLARDPYCAW--DQACSRYTASSKRRSRRQD 556
 Qy 557 IERGN 561
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 Db 557 VRHGN 561

RESULT 14

I48748

semaphorin E - mouse

C;Species: Mus musculus (house mouse)

C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 24-Sep-1999

C;Accession: I48748

R;Puschel, A.W.; Adams, R.H.; Betz, H.

Neuron 14, 941-948, 1995

A;Title: Murine semaphorin D/collapsin is a member of a diverse gene family and creates domains inhibitory for axonal extension.

A;Reference number: I48744; MUID:95267431; PMID:7748561

A;Accession: I48748

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-751 <RES>

A;Cross-references: EMBL:X85994; NID:g854331; PIDN:CAA59986.1; PID:g854332

C;Genetics:

A;Gene: semE

C;Superfamily: semaphorin

Query Match 13.5%; Score 737; DB 2; Length 751;

Best Local Similarity 31.3%; Pred. No. 3e-41;

Matches 187; Conservative 103; Mismatches 234; Indels 74; Gaps 18;

Qy 24 SEPISISHGNYTKQYPVFGHKPGRNTTQRHRLDIQMIMI--MNGTLYIAARDHIYTVDI 81
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 Db 42 SEYFSLSH-----QQLDYRILLMDEDQDRIYVGSKDHLISLNI 79
 Qy 82 DTSHTEEIYCSKKLTWKSQADVDTCRMKGKHKDE-CHNFIKVLLKKNDALFVCGTNAF 140
 : | : : | : | : | : | | | | : : : : | | : | : | : | : | : | : | :
 Db 80 NNISQEPL----SVFWPASTIKVEECKMAGKDPHGCNGFVRVIQTENRTHLYVCGSGAF 135

QY 141 NPSC----RNYKMDTLEPFGDEF-----SGMARCPYDAKHANVALFADGKLYSATVT 188
 :| | : : | : || || :: |:: : :|
 Db 136 SPVCTYLNRGRSE-----DQVFMIDSKCESGKGRCSEFNPVNVTVSVMINEELFSGMYI 189

QY 189 DFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQA-----VDYGD-YIYFFFREIAV 241
 ||: || |:|| : ||| :|:|||| || || | | :|:|:|
 Db 190 DFMGTDAAIFRSLTKRMLRTDQHNSKWLSEPMFVDAHVIPDGTDPNDAKVYFFFKERLT 249

QY 242 EYNTMGKVVFPRAQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDS--HFYFNILQAV 299
 : | : :|::| || || || | :|:|:| || | : :|: |
 Db 250 DNNRSTKQIHSMIARICPNDTGG-QRSLVNKWTTFKARLVCSVTDEDGPETHFDELEDV 308

QY 300 TDVIRINGR-DVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVPD 358
 : | | :| :| : |||| | : || :| | | :: |:
 Db 309 FLLETDNPRRTLVIYGFITSSSVFKGSAVCVYHLSDIQTVFNGPFAHKEGPNHQLISY-Q 367

QY 359 ERVPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRY 418
 |:| |||| | : | :|:| : ||: |||| :: | || :| |
 Db 368 GRIPYPRPGTCPGGAFTPNMRTTKDFPDDVVTFIRNHPLMYNSISPIHRRPLIVRIGTDY 427

QY 419 RLTKIAVDTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLNDSLFLLEEMSVYNSEKCS 478
 : ||||| : |:|:|:| : | : || : | ||| : :
 Db 428 KYTKIAVDRVNAADGRYHVLFLGTDRTGVQKVVLPTNSS-ASGELILEELEVFKNH--- 483

QY 479 YDGVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRCERHGKCKKTCIASRDPYCGWIKE 538
 | |:: ||: : | :| | | :| | :| ||| | :
 Db 484 -----VPITTEISSKKQQLYVSSNEGVSQVSLHRCHIYGTACADCCCLARDPYCAW--D 535

QY 539 GGACSHLSP-NSRLTFEQDIERGNTDGLGDCHNSFVALNGHSSSLPSTTTSDSTAQE 595
 | :|| | : ||: || | | : : : : :|| |
 Db 536 GHSCSRFYPTGKRSSRRQDVRHGNP--LTQCRGFNLKAYRNAAEIVQYGVRRNNSTFLE 591

RESULT 15

S66498

M-sema F protein precursor - mouse

C;Species: Mus musculus (house mouse)

C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 24-Nov-1999

C;Accession: S66498

R;Inagaki, S.; Furuyama, T.; Iwahashi, Y.

FEBS Lett. 370, 269-272, 1995

A;Title: Identification of a member of mouse semaphorin family.

A;Reference number: S66498; MUID:95385809; PMID:7656991

A;Accession: S66498

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-834 <INA>

A;Cross-references: EMBL:S79463; NID:g1110598; PIDN:AAB35184.1; PID:g1110599

C;Superfamily: semaphorin

F;1-21/Domain: signal sequence #status predicted <SIG>

F;22-834/Product: M-sema F protein #status predicted <MAT>

Query Match 12.7%; Score 692; DB 2; Length 834;

Best Local Similarity 26.0%; Pred. No. 3.7e-38;

Matches 232; Conservative 131; Mismatches 326; Indels 204; Gaps 34;

QY 65 NGTLYIAARDHIYTVDIDTSHTEEIYCSKKLTWKSQRQADVDTCRMKGK-HKDECHNFIKV 123

Db	62	SGLLYVGAREALFAFSV-----EALELQGAISWEAPAEKKIECTQKGKSNQTECFNFIRF	116
Qy	124	LLKKND DALFVCGTNAFNPSCRNYKMDTLEPFGDEF-SGMARCPYDAKHANVALFADGKL	182
Db	117	LQPYNSSHLVCGTYAFQPKCTYINMLTFTLDRAEFEDGKGKCPYDPAKGHTGLLDVGEL	176
Qy	183	YSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQA-----VDYGDYI	232
Db	177	YSATLNNFLGTPEVILRYMGTHHSIKT-EYLAFWLNPHFVGSAFVPESVGSFTGDDDKI	235
Qy	233	YFFFREIAVEYNTMGKVVFPRAVQCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDSHFY	292
Db	236	YFFFSERAVEYDCYSEQVVARVARVCKGDMGGA-RTLQKKWTTFLKARLVCSAP-DWKVY	293
Qy	293	FNILQAVTDVIRINGRDVV-LATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDS	351
Db	294	FNQLKAVHTLRGASWHNTTFFGVFQARWGDMDLSAVCEYQLEQIQQVFEGPYKEYSEQAQ	353
Qy	352	TWTPVPDERVPKPRPGCCAGSSSLER-YATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPW	410
Db	354	KWARYTDP-VSPRPGSCINNWHRDNGYTSSLELPDNTLNFIKKHPLMEDQVKPRLGRPL	412
Qy	411	FLRTMVRYRLTKIAVDTAAG-PYQNHTVVFLGSEKGIILKFLARIGNSGFLNDSL-----	464
Db	413	LVKKNTNF--THVVADRVPLDGATYTVLFIGTGDGWLLKAV-----SLGPWIH	459
Qy	465	FLEEMSVYNSEKCSYDGVEDKRIMGMLDRASSSLYVAFSTCVIKVPLGRRCERHGKCKKT	524
Db	460	MVEELQVFDQEP-----VESLVSQSCKVLFAGSRSQVLVQLSLADCTKYRFC-VD	508
Qy	525	CIASRPYCGWIKEGGAC-----SHLS--PNSRLTFEQDIER-----	559
Db	509	CVLARDPYCAWNVNTSRCVATTSGRSGSFLVQHVANLDTSKMCNQYGIKKVRSIPKNITV	568
Qy	560	-GNTDGLGDCHNSFVALNGH---SSSLLPSTTTSDSTAQEGYESRGGMLDWKHLLDSPDS	615
Db	569	VSGTDLVLPCHLSSNLAHAHWTFGSQDLPAEQPGSFLYDTGLQALVVM-----	616
Qy	616	TDPLGAVSSH-----HQDKKG--VIRESYLKG-----HDQLVPVTL LAI AVILAFV	660
Db	617	----AAQSRHSGPYRCYSEEQGTRLAAESYLVAVVAGSSVTLEARAPLENLGLVWLAVVA	672
Qy	661	MGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRGSMSSVTKL SGLFGDTQSKDPKPE	720
Db	673	LGAVCL-VLLLLVLSLRRR-----LREELE-----KGAKAS-----ER	704
Qy	721	AILTPLMHNGKLATPGNTAKMLIKADQHHLDTALPTPESTPTLQQKRKPSRGSREW---	777
Db	705	TLVYPL-----ELPKEPASPPF--RPGPETDEKLWDPV	735
Qy	778	-----ERNQNLINACTKDMPPMGSPVIPTDLPLRASPSHIPSVVVLPI TQQGYQHEYVDQ	832
Db	736	GYYSYSDGSLKIVPGHARCQPGGGPPSPPPGIPGQPLPS--PTRLHLGGGRNSNANGYVR-	792
Qy	833	PKMSEVAQMALEDQAATLEYKTIKEHLSSKSPNHGVNLVENLDSLPPKVPQRE	885

Db 793 -----LQLGGEDRGGS-----GHPLPELADELRRKLQQRQ 822

Search completed: March 24, 2004, 13:17:10
Job time : 33.8439 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 24, 2004, 13:14:29 ; Search time 74.7731 Seconds
(without alignments)
3567.110 Million cell updates/sec

Title: US-09-856-681A-2
Perfect score: 5450
Sequence: 1 MRSEALLLYFTLLHFAGAGF.....PPKPSFAPLSTSMKPNDACT 1030

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1049977 seqs, 258955339 residues

Total number of hits satisfying chosen parameters: 1049977

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query	
No.	Score Match Length DB ID	Description

1	5450	100.0	1030	12	US-10-016-248-63	Sequence 63, Appl
2	5431.5	99.7	1047	12	US-10-403-676-48	Sequence 48, Appl
3	5431.5	99.7	1047	15	US-10-449-548-48	Sequence 48, Appl
4	5422.5	99.5	1047	10	US-09-957-187-85	Sequence 85, Appl
5	5422.5	99.5	1047	12	US-10-403-676-14	Sequence 14, Appl
6	5422.5	99.5	1047	15	US-10-449-548-14	Sequence 14, Appl
7	5368	98.5	1018	12	US-10-403-676-28	Sequence 28, Appl
8	5368	98.5	1018	15	US-10-449-548-28	Sequence 28, Appl
9	5349.5	98.2	1035	12	US-10-403-676-18	Sequence 18, Appl
10	5349.5	98.2	1035	15	US-10-449-548-18	Sequence 18, Appl
11	5134.5	94.2	998	12	US-10-403-676-20	Sequence 20, Appl
12	5134.5	94.2	998	15	US-10-449-548-20	Sequence 20, Appl
13	5113.5	93.8	981	12	US-10-403-676-30	Sequence 30, Appl
14	5113.5	93.8	981	15	US-10-449-548-30	Sequence 30, Appl
15	5109.5	93.8	971	12	US-10-403-676-46	Sequence 46, Appl
16	5109.5	93.8	971	15	US-10-449-548-46	Sequence 46, Appl
17	4921	90.3	939	10	US-09-957-187-4	Sequence 4, Appli
18	4921	90.3	939	12	US-10-403-676-32	Sequence 32, Appl
19	4921	90.3	939	15	US-10-449-548-32	Sequence 32, Appl
20	4590.5	84.2	884	10	US-09-957-187-6	Sequence 6, Appli
21	4346.5	79.8	888	12	US-10-016-248-64	Sequence 64, Appl
22	3373	61.9	630	10	US-09-957-187-30	Sequence 30, Appl
23	3368	61.8	861	12	US-10-403-676-52	Sequence 52, Appl
24	3368	61.8	861	15	US-10-449-548-52	Sequence 52, Appl
25	3367.5	61.8	636	12	US-10-403-676-36	Sequence 36, Appl
26	3367.5	61.8	636	15	US-10-449-548-36	Sequence 36, Appl
27	3363	61.7	666	12	US-10-403-676-56	Sequence 56, Appl
28	3363	61.7	666	15	US-10-449-548-56	Sequence 56, Appl
29	3362	61.7	626	10	US-09-957-187-83	Sequence 83, Appl
30	3362	61.7	626	12	US-10-403-676-34	Sequence 34, Appl
31	3362	61.7	626	15	US-10-449-548-34	Sequence 34, Appl
32	3351.5	61.5	649	12	US-10-403-676-50	Sequence 50, Appl
33	3351.5	61.5	649	15	US-10-449-548-50	Sequence 50, Appl
34	3349.5	61.5	878	12	US-10-403-676-54	Sequence 54, Appl
35	3349.5	61.5	878	15	US-10-449-548-54	Sequence 54, Appl
36	3285.5	60.3	640	12	US-10-403-676-16	Sequence 16, Appl
37	3285.5	60.3	640	15	US-10-449-548-16	Sequence 16, Appl
38	2627	48.2	497	12	US-10-403-676-24	Sequence 24, Appl
39	2627	48.2	497	15	US-10-449-548-24	Sequence 24, Appl
40	2545	46.7	479	12	US-10-403-676-26	Sequence 26, Appl
41	2545	46.7	479	15	US-10-449-548-26	Sequence 26, Appl
42	2349.5	43.1	1088	12	US-10-016-248-20	Sequence 20, Appl
43	2335	42.8	1035	12	US-10-016-248-12	Sequence 12, Appl
44	2330	42.8	442	12	US-10-403-676-22	Sequence 22, Appl
45	2330	42.8	442	15	US-10-449-548-22	Sequence 22, Appl

ALIGNMENTS

RESULT 1
 US-10-016-248-63
 ; Sequence 63, Application US/10016248
 ; Publication No. US20040033491A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Alsobrook et al.

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; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-218
; CURRENT APPLICATION NUMBER: US/10/016,248
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/254,329
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/291,037
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 60/255,648
; PRIOR FILING DATE: 2000-12-14
; PRIOR APPLICATION NUMBER: 60/297,173
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: 60/309,258
; PRIOR FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: 60/326,393
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/315,639
; PRIOR FILING DATE: 2001-08-29
; NUMBER OF SEQ ID NOS: 167
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 63
; LENGTH: 1030
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-016-248-63
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Query Match          100.0%; Score 5450; DB 12; Length 1030;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1030; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db      1 MRSEALLLYFTLLHFAGAGFPEDSEPISSHGNYTKQYPVFVGHKPGRNTTQRHRLDIQM 60

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Db     61 IMIMNGTLYIAARDHIYTVDIDTSHTEEIYCSKKLTWKSQADVDTCRMKGKHKDECHNF 120

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Db    121 IKVLLKKND DALFVCGTNAFNPSCRNYKMDTLEPFGDEFSGMARCPYDAKHANVALFADG 180

Qy    181 KLYSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYFFFREIA 240
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Qy    241 VEYNTMGKVVFPRVAQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDSHFYFNILQAVT 300
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Db    241 VEYNTMGKVVFPRVAQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDSHFYFNILQAVT 300

Qy    301 DVIRINGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVPDER 360
|
Db    301 DVIRINGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVPDER 360

Qy    361 VPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRL 420
|
Db    361 VPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRL 420
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Qy 421 TKIAVDTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLNDSLFLLEEMSVYNSEKCSYD 480
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Qy 481 GVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRGERHGKCKKTCIASRDPYCGWKEGG 540
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Qy 541 ACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALNGHSSSLPSTTTSDSTAQEGYESR 600
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Qy 661 MGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRRGSMSSVTKLSGLFGDTQSKDPKPE 720
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Qy 781 QNLINACTKDMPPMGSPVIPTDLPLRASPSHIPSVVLPITQQGYQHEYVDQPKMSEVAQ 840
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Qy 841 MALEDQAATLEYKTIKEHLSSKSPNHGVNLVENLDSLPPKVPQREASLGPPGASLSQTGL 900
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 Db 841 MALEDQAATLEYKTIKEHLSSKSPNHGVNLVENLDSLPPKVPQREASLGPPGASLSQTGL 900

Qy 901 SKRLEMHHSSSYGVVDYKRSYPTNSLTRSHQATTLKRNTNTSSNSSHLSRNQSFGRGDNPP 960
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 Db 901 SKRLEMHHSSSYGVVDYKRSYPTNSLTRSHQATTLKRNTNTSSNSSHLSRNQSFGRGDNPP 960

Qy 961 PAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRTPSLKPDPVPPKPSFAPLS 1020
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 Db 961 PAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRTPSLKPDPVPPKPSFAPLS 1020

Qy 1021 TSMKPNDACT 1030
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 Db 1021 TSMKPNDACT 1030

RESULT 2

US-10-403-676-48

; Sequence 48, Application US/10403676

; Publication No. US20040029150A1

; GENERAL INFORMATION:

; APPLICANT: Alsobrook II, John

; APPLICANT: Anderson, David W.

; APPLICANT: Boldog, Ferenc L.

; APPLICANT: Burgess, Catherine E.

; APPLICANT: Casman, Stacie J.

; APPLICANT: Edinger, Shlomit R.

; APPLICANT: Gerlach, Valerie L.
 ; APPLICANT: Grosse, William M.
 ; APPLICANT: Guo, Xiaojia
 ; APPLICANT: Gusev, Vladimir Y.
 ; APPLICANT: Ji, Weizhen
 ; APPLICANT: LaRochelle, William J.
 ; APPLICANT: Lepley, Denise M.
 ; APPLICANT: Li, Li
 ; APPLICANT: Liu, Xiaohong
 ; APPLICANT: MacDougall, John R.
 ; APPLICANT: Malyankar, Uriel M.
 ; APPLICANT: Millet, Isabelle
 ; APPLICANT: Padigar, Muralidhara
 ; APPLICANT: Patturajan, Meera
 ; APPLICANT: Peyman, John A.
 ; APPLICANT: Rastelli, Luca
 ; APPLICANT: Reiger, Daniel
 ; APPLICANT: Rothenberg, Mark E.
 ; APPLICANT: Shimkets, Richard A.
 ; APPLICANT: Stone, David J.
 ; APPLICANT: Taupier, Raymond J.
 ; APPLICANT: Vernet, Corine
 ; APPLICANT: Zerhusen, Bryan D.
 ; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME,
 AND METHODS OF USE
 ; FILE REFERENCE: 21402-573B
 ; CURRENT APPLICATION NUMBER: US/10/403,676
 ; CURRENT FILING DATE: 2003-03-31
 ; PRIOR APPLICATION NUMBER: 60/123,667
 ; PRIOR FILING DATE: 1999-03-09
 ; PRIOR APPLICATION NUMBER: 09/520,781
 ; PRIOR FILING DATE: 2000-03-08
 ; PRIOR APPLICATION NUMBER: 09/957,187
 ; PRIOR FILING DATE: 2001-09-19
 ; PRIOR APPLICATION NUMBER: 60/371,002
 ; PRIOR FILING DATE: 2002-04-09
 ; PRIOR APPLICATION NUMBER: 60/127,352
 ; PRIOR FILING DATE: 1999-04-01
 ; PRIOR APPLICATION NUMBER: 09/538,092
 ; PRIOR FILING DATE: 2000-03-29
 ; PRIOR APPLICATION NUMBER: 09/604,286
 ; PRIOR FILING DATE: 2000-06-22
 ; PRIOR APPLICATION NUMBER: 60/140,584
 ; PRIOR FILING DATE: 1999-06-23
 ; PRIOR APPLICATION NUMBER: 60/370,381
 ; PRIOR FILING DATE: 2002-04-05
 ; PRIOR APPLICATION NUMBER: 60/384,297
 ; PRIOR FILING DATE: 2002-05-30
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 179
 ; SOFTWARE: CuraSeqList version 0.1
 ; SEQ ID NO 48
 ; LENGTH: 1047
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-403-676-48

Query Match 99.7%; Score 5431.5; DB 12; Length 1047;
Best Local Similarity 98.4%; Pred. No. 0;
Matches 1030; Conservative 0; Mismatches 0; Indels 17; Gaps 1;

Qy	1	MRSEALLLYFTLLHFAGAGFPEDSEPISISHGNYTKQYPVFVGHKPGRNTTQRHRLDIQM	60
Db	1	MRSEALLLYFTLLHFAGAGFPEDSEPISISHGNYTKQYPVFVGHKPGRNTTQRHRLDIQM	60
Qy	61	IMIMNGTLYIAARDHIYTVDIDTSHTEEIYCSKKLTWKSQRQADVDCRMKGKHKDECHNF	120
Db	61	IMIMNGTLYIAARDHIYTVDIDTSHTEEIYCSKKLTWKSQRQADVDCRMKGKHKDECHNF	120
Qy	121	IKVLLKKND DALFVCGTNAFNPS CRNYKMDTLEPFGDEFSGMARCPYDAKHANVALFADG	180
Db	121	IKVLLKKND DALFVCGTNAFNPS CRNYKMDTLEPFGDEFSGMARCPYDAKHANVALFADG	180
Qy	181	KLYSATVTDFLAIDAVIYRSLGESPTLRV KHDSKW LKEPYFVQAVDYGDIYFFFREIA	240
Db	181	KLYSATVTDFLAIDAVIYRSLGESPTLRV KHDSKW LKEPYFVQAVDYGDIYFFFREIA	240
Qy	241	VEYNTMGKVVFPRVAQVCKNDMGGSQ RVLEKQWTSFLKARLNCSVPGD SHFYFNILQAVT	300
Db	241	VEYNTMGKVVFPRVAQVCKNDMGGSQ RVLEKQWTSFLKARLNCSVPGD SHFYFNILQAVT	300
Qy	301	DVIRINGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPV PDER	360
Db	301	DVIRINGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPV PDER	360
Qy	361	VPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVR YRL	420
Db	361	VPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVR YRL	420
Qy	421	TKIAVDTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLNDSL FLEEMSVYNSEKCSYD	480
Db	421	TKIAVDTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLNDSL FLEEMSVYNSEKCSYD	480
Qy	481	GVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGR CERH GKCKKTCIASRDPYCGW IKEGG	540
Db	481	GVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGR CERH GKCKKTCIASRDPYCGW IKEGG	540
Qy	541	ACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALN-----GHSS SLL	583
Db	541	ACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALNDISTPLPDNEMSYNTVYGHSS SLL	600
Qy	584	PSTTTSDSTAQEGYESRGGMLDWKHLLDSPDSTDPLGAVSSHNHQDKKGVIRESY LKGHD	643
Db	601	PSTTTSDSTAQEGYESRGGMLDWKHLLDSPDSTDPLGAVSSHNHQDKKGVIRESY LKGHD	660
Qy	644	QLVPVTLLAIAVILAFVMGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSR RGSMS SVT	703
Db	661	QLVPVTLLAIAVILAFVMGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSR RGSMS SVT	720
Qy	704	KL SGLFGDTQSKDPKPEAILTPLMHNGKLATPGNTAKMLIKADQHHLDTALPTPE STPT	763
Db	721	KL SGLFGDTQSKDPKPEAILTPLMHNGKLATPGNTAKMLIKADQHHLDTALPTPE STPT	780
Qy	764	LQQKRKPSRGSREWERNQN LINACTKDMPPMGSPVIPTDLPLRASPSHIPSVV VLPITQQ	823

Db	781		LQQKRKPSRGSREWERNQNINACTKDMPPMGSPVIPTDLPLRASPSHIPSVVVLPIITQQ	840
Qy	824		GYQHEYVDQPKMSEVAQMALEDQAATLEYKTIKEHLSSKSPNHGMVNLVENLDSLPPKVPQ	883
Db	841		GYQHEYVDQPKMSEVAQMALEDQAATLEYKTIKEHLSSKSPNHGMVNLVENLDSLPPKVPQ	900
Qy	884		REASLGPPGASLSQTGLSKRLEMHHSSSYGVVDYKRSYPTNSLTRSHQATTLKRNTNSSN	943
Db	901		REASLGPPGASLSQTGLSKRLEMHHSSSYGVVDYKRSYPTNSLTRSHQATTLKRNTNSSN	960
Qy	944		SSHLSRNQSFGRGDNPPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRT	1003
Db	961		SSHLSRNQSFGRGDNPPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRT	1020
Qy	1004		PSLKPDPVPPKPSFAPLSTSMKPNDACT	1030
Db	1021		PSLKPDPVPPKPSFAPLSTSMKPNDACT	1047

RESULT 3

US-10-449-548-48

; Sequence 48, Application US/10449548

; Publication No. US20040018977A1

; GENERAL INFORMATION:

; APPLICANT: Alvarez, Enrique

; APPLICANT: Anderson, David W.

; APPLICANT: Dhanabal, Mohanraj

; APPLICANT: Khramtsov, Nikolai V.

; APPLICANT: LaRochelle, William J.

; APPLICANT: Li, Li

; APPLICANT: Lichenstein, Henri

; APPLICANT: Ooi, Chean Eng

; APPLICANT: Padigar, Muralidhara

; APPLICANT: Shimkets, Richard A.

; APPLICANT: Zhong, Mei

; TITLE OF INVENTION: SEMAPHORIN-LIKE PROTEINS AND METHODS OF USING SAME

; FILE REFERENCE: 15966-540CIP2

; CURRENT APPLICATION NUMBER: US/10/449,548

; CURRENT FILING DATE: 2003-05-30

; PRIOR APPLICATION NUMBER: 09/520,781

; PRIOR FILING DATE: 2000-03-03

; PRIOR APPLICATION NUMBER: 60/123,667

; PRIOR FILING DATE: 1999-03-09

; PRIOR APPLICATION NUMBER: 60/234,082

; PRIOR FILING DATE: 2000-09-20

; PRIOR APPLICATION NUMBER: 60/233,798

; PRIOR FILING DATE: 2000-09-19

; PRIOR APPLICATION NUMBER: 60/174,485

; PRIOR FILING DATE: 2000-01-04

; PRIOR APPLICATION NUMBER: 10/403,676

; PRIOR FILING DATE: 2003-03-31

; PRIOR APPLICATION NUMBER: 60/371,002

; PRIOR FILING DATE: 2002-04-09

; PRIOR APPLICATION NUMBER: 60/384,798

; PRIOR FILING DATE: 2002-05-30

; PRIOR APPLICATION NUMBER: 60/402,407

; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 60/443,062
; PRIOR FILING DATE: 2003-01-28
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 48
; LENGTH: 1047
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-449-548-48

Query Match 99.7%; Score 5431.5; DB 15; Length 1047;
Best Local Similarity 98.4%; Pred. No. 0;
Matches 1030; Conservative 0; Mismatches 0; Indels 17; Gaps 1;

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Qy      1 MRSEALLLYFTLLHFAGAGFPEDSEPISISHGNYTKQYPVFVGHKPGRNTTQRHRLDIQM 60
          |||
Db      1 MRSEALLLYFTLLHFAGAGFPEDSEPISISHGNYTKQYPVFVGHKPGRNTTQRHRLDIQM 60

Qy     61 IMIMNGTLYIAARDHIYTVDIDTSHTEEIYCSKKLTWKSQRQADVDTCRMKGKHKDECHNF 120
          |||
Db     61 IMIMNGTLYIAARDHIYTVDIDTSHTEEIYCSKKLTWKSQRQADVDTCRMKGKHKDECHNF 120

Qy    121 IKVLLKKND DALFVCGTNAFNPS CRNYKMDTLEPFGDEFSGMARCPYDAKHANVALFADG 180
          |||
Db    121 IKVLLKKND DALFVCGTNAFNPS CRNYKMDTLEPFGDEFSGMARCPYDAKHANVALFADG 180

Qy    181 KLYSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYFFFREIA 240
          |||
Db    181 KLYSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYFFFREIA 240

Qy    241 VEYNTMGKVVFPRVAQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPGD SHFYFNILQAVT 300
          |||
Db    241 VEYNTMGKVVFPRVAQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPGD SHFYFNILQAVT 300

Qy    301 DVIRINGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVPDER 360
          |||
Db    301 DVIRINGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVPDER 360

Qy    361 VPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRL 420
          |||
Db    361 VPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRL 420

Qy    421 TKIAVDTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLNDSL FLEEMSVYNSEKCSYD 480
          |||
Db    421 TKIAVDTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLNDSL FLEEMSVYNSEKCSYD 480

Qy    481 GVEDKRIMGMLDRASSSLYVAFSTCVIKVPLGR CERHGKCKKTCIASRDPYCGWKEGG 540
          |||
Db    481 GVEDKRIMGMLDRASSSLYVAFSTCVIKVPLGR CERHGKCKKTCIASRDPYCGWKEGG 540

Qy    541 ACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALN-----GHSSSSL 583
          |||
Db    541 ACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALNDISTPLPDNEMSYNTVYGHSSSSL 600

Qy    584 PSTTTSDSTAQEGYESRGGMLDWKHL LDDSPDSTDP LGAVSSH NHQDKKGVIRESYLK GHD 643
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Db	601	PSTTTSDSTAQEGYESRGGMLDWKHLSDPDSTPLGAVSSHNHQDKKGVIRESYLKGH	660
Qy	644	QLVPVTLIAIVILAFVMGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRGSMSSVT	703
Db	661	QLVPVTLIAIVILAFVMGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRGSMSSVT	720
Qy	704	KLSGLFGDTQSKDPKPEAILTPLMHNGKLATPGNTAKMLIKADQHHLDTALPTPESTPT	763
Db	721	KLSGLFGDTQSKDPKPEAILTPLMHNGKLATPGNTAKMLIKADQHHLDTALPTPESTPT	780
Qy	764	LQQKRKPSRGSREWERNQNLINACTKDMPPMGSPVIPTDLPLRASPSHIPSVVLPITQQ	823
Db	781	LQQKRKPSRGSREWERNQNLINACTKDMPPMGSPVIPTDLPLRASPSHIPSVVLPITQQ	840
Qy	824	GYQHEYVDQPKMSEVAQMALEDQAATLEYKTIKEHLSSKSPNHGVLNLDLPPKVPQ	883
Db	841	GYQHEYVDQPKMSEVAQMALEDQAATLEYKTIKEHLSSKSPNHGVLNLDLPPKVPQ	900
Qy	884	REASLGPPGASLSQTGLSKRLEMHHSSSYGVYDKRSYPTNSLTRSHQATTLKRNTNSSN	943
Db	901	REASLGPPGASLSQTGLSKRLEMHHSSSYGVYDKRSYPTNSLTRSHQATTLKRNTNSSN	960
Qy	944	SSHLSRNQSFGRGDNPPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRT	1003
Db	961	SSHLSRNQSFGRGDNPPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRT	1020
Qy	1004	PSLKPDPVPPKPSFAPLSTSMKPNDACT	1030
Db	1021	PSLKPDPVPPKPSFAPLSTSMKPNDACT	1047

RESULT 4

US-09-957-187-85

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; Sequence 85, Application US/09957187
; Publication No. US20030054514A1
; GENERAL INFORMATION:
; APPLICANT: Shimkets, Richard A.
; APPLICANT: LaRochelle, William
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES AND PROTEINS ENCODED THEREBY
; FILE REFERENCE: 15966-540 CIP
; CURRENT APPLICATION NUMBER: US/09/957,187
; CURRENT FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 60/123,667
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: 09/520,781
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: 60/234,082
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: 60/233,798
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 60/174,485
; PRIOR FILING DATE: 2000-01-04
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 85
; LENGTH: 1047
; TYPE: PRT

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; ORGANISM: Homo sapiens
US-09-957-187-85

Query Match 99.5%; Score 5422.5; DB 10; Length 1047;
Best Local Similarity 98.3%; Pred. No. 0;
Matches 1029; Conservative 0; Mismatches 1; Indels 17; Gaps 1;

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Db      1 MRSEALLLYFTLLHFAGAGFPEDSEPISISHCNYTKQYPVFVGHKPGRNTTQRHRLDIQM 60

Qy     61 IMIMNGTLYIAARDHIYTVDIDTSHTEEIYCSKKLTWKSQRQADVDCRMKGKHKDECHNF 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 IMIMNGTLYIAARDHIYTVDIDTSHTEEIYCSKKLTWKSQRQADVDCRMKGKHKDECHNF 120

Qy    121 IKVLLKKNDALFVCGTNAFNPSCRNYKMDTLEPFGDEFSGMARCPYDAKHANVALFADG 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 IKVLLKKNDALFVCGTNAFNPSCRNYKMDTLEPFGDEFSGMARCPYDAKHANVALFADG 180

Qy    181 KLYSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYFFFREIA 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 KLYSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYFFFREIA 240

Qy    241 VEYNTMGKVVFPRVAQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDSHFYFNILQAVT 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 VEYNTMGKVVFPRVAQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDSHFYFNILQAVT 300

Qy    301 DVIRINGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVPDER 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 DVIRINGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVPDER 360

Qy    361 VPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRL 420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 VPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRL 420

Qy    421 TKIAVDTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLNDSLFLEEMSVYNSEKCSYD 480
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 TKIAVDTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLNDSLFLEEMSVYNSEKCSYD 480

Qy    481 GVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRCERHGKCKKTCIASRDPYCGWKEGG 540
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 GVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRCERHGKCKKTCIASRDPYCGWKEGG 540

Qy    541 ACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALN-----GHSSSLL 583
        ||||||||||||||||||||||||||||||||||||||||||||
Db    541 ACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALNDISTPLPDNEMSYNTVYGHSSSLL 600

Qy    584 PSTTTSDSTAQEGYESRGGMLDWKHLSDPDSTDPLGAVSSHNHQDKKGVIRESYLKGH 643
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 PSTTTSDSTAQEGYESRGGMLDWKHLSDPDSTDPLGAVSSHNHQDKKGVIRESYLKGH 660

Qy    644 QLVPVTLLAIAVILAFVMGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRRGSMSSVT 703
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 QLVPVTLLAIAVILAFVMGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRRGSMSSVT 720

Qy    704 KLSGLFGDTQSKDPKPEAILTPLMHNGKLATPGNTAKMLIKADQHHLDTALPTPESTPT 763
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db	721	KLSGLFGDTQSKDPKPEAILTPLMHNGKLATPGNTAKMLIKADQHHLDLTALPTPESTPT	780
Qy	764	LQQKRKPSRGSREWERNQNLINACTKDMPPMGSPVIPTDLPLRASPSHIPSVVVLPIITQQ	823
Db	781	LQQKRKPSRGSREWERNQNLINACTKDMPPMGSPVIPTDLPLRASPSHIPSVVVLPIITQQ	840
Qy	824	GYQHEYVDQPKMSEVAQMALEDQAATLEYKTIKEHLSSKSPNHGVLNLDLPPKVPQ	883
Db	841	GYQHEYVDQPKMSEVAQMALEDQAATLEYKTIKEHLSSKSPNHGVLNLDLPPKVPQ	900
Qy	884	REASLGPPGASLSQTGLSKRLEMHHSSSYGVYKRSYPTNSLTRSHQATTLKRNTNSSN	943
Db	901	REASLGPPGASLSQTGLSKRLEMHHSSSYGVYKRSYPTNSLTRSHQATTLKRNTNSSN	960
Qy	944	SSHLSRNQSFGRGDNPPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRT	1003
Db	961	SSHLSRNQSFGRGDNPPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRT	1020
Qy	1004	PSLKPDPVPPKPSFAPLSTSMKPNDACT	1030
Db	1021	PSLKPDPVPPKPSFAPLSTSMKPNDACT	1047

RESULT 5

US-10-403-676-14

; Sequence 14, Application US/10403676

; Publication No. US20040029150A1

; GENERAL INFORMATION:

; APPLICANT: Alsobrook II, John
; APPLICANT: Anderson, David W.
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Grosse, William M.
; APPLICANT: Guo, Xiaojia
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Ji, Weizhen
; APPLICANT: LaRochelle, William J.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Li, Li
; APPLICANT: Liu, Xiaohong
; APPLICANT: MacDougall, John R.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Millet, Isabelle
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Patturajan, Meera
; APPLICANT: Peyman, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Reiger, Daniel
; APPLICANT: Rothenberg, Mark E.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Stone, David J.
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Vernet, Corine
; APPLICANT: Zerhusen, Bryan D.

```

; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME,
AND METHODS OF USE
; FILE REFERENCE: 21402-573B
; CURRENT APPLICATION NUMBER: US/10/403,676
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: 60/123,667
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: 09/520,781
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 09/957,187
; PRIOR FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/371,002
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 09/538,092
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 09/604,286
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 60/140,584
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 60/370,381
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/384,297
; PRIOR FILING DATE: 2002-05-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 179
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 14
; LENGTH: 1047
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-403-676-14

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Query Match          99.5%; Score 5422.5; DB 12; Length 1047;
Best Local Similarity 98.3%; Pred. No. 0;
Matches 1029; Conservative 0; Mismatches 1; Indels 17; Gaps 1;

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Qy      1 MRSEALLLYFTLLHFAGAGFPEDSEPI SISHGNYTKQYPVFVGHKPGRNTTQRHRLDIQM 60
        |||||||
Db      1 MRSEALLLYFTLLHFAGAGFPEDSEPI SISHCNYTKQYPVFVGHKPGRNTTQRHRLDIQM 60
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Qy     61 IMIMNGTLYIAARDHIYTVDIDTSHTEEIYCSKKLTWKS RQADVDTCRMKGKHKDECHNF 120
        |||||||
Db     61 IMIMNGTLYIAARDHIYTVDIDTSHTEEIYCSKKLTWKS RQADVDTCRMKGKHKDECHNF 120
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Qy    121 IKVLLKKND DALFVCGTNAFNPSCRNYKMDTLEPFGDEFSGMARCPYDAKHANVALFADG 180
        |||||||
Db    121 IKVLLKKND DALFVCGTNAFNPSCRNYKMDTLEPFGDEFSGMARCPYDAKHANVALFADG 180
        |||||||

Qy    181 KLYSATVTDFLAIDAVIYRSLGESPTLR TVKHDSKWLKEPYFVQAVDYGDIYFFFREIA 240
        |||||||
Db    181 KLYSATVTDFLAIDAVIYRSLGESPTLR TVKHDSKWLKEPYFVQAVDYGDIYFFFREIA 240
        |||||||

Qy    241 VEYNTMGKVVFP RVAQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDSHFYFNILQAVT 300
        |||||||
Db    241 VEYNTMGKVVFP RVAQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDSHFYFNILQAVT 300
        |||||||

```

Qy	301	DVIRINGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVPDER	360
Db	301	DVIRINGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVPDER	360
Qy	361	VPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRL	420
Db	361	VPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRL	420
Qy	421	TKIAVDTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLNDSLFLEEMSVYNSEKCSYD	480
Db	421	TKIAVDTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLNDSLFLEEMSVYNSEKCSYD	480
Qy	481	GVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGR CERHGKCKKTCIASRDPYCGWIKEGG	540
Db	481	GVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGR CERHGKCKKTCIASRDPYCGWIKEGG	540
Qy	541	ACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALN-----GHSSSLL	583
Db	541	ACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALNDISTPLPDNEMSYNTVYGHSSSLL	600
Qy	584	PSTTTSDSTAQEGYESRGGMLDWKHLSDPDSTDPLGAVSSHNHQDKKGVIRESYLKGH	643
Db	601	PSTTTSDSTAQEGYESRGGMLDWKHLSDPDSTDPLGAVSSHNHQDKKGVIRESYLKGH	660
Qy	644	QLVPVTLIAIAVILAFVMGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRGSMSSVT	703
Db	661	QLVPVTLIAIAVILAFVMGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRGSMSSVT	720
Qy	704	KLSGLFGDTQSKDPKPEAILTPLMHNGKLATPGNTAKMLIKADQHHLDTALPTPESTPT	763
Db	721	KLSGLFGDTQSKDPKPEAILTPLMHNGKLATPGNTAKMLIKADQHHLDTALPTPESTPT	780
Qy	764	LQQKRKPSRGSREWERNQNLINACTKDMPPMGSPVIPTDLPLRASPSHIPSVVVLPTQQ	823
Db	781	LQQKRKPSRGSREWERNQNLINACTKDMPPMGSPVIPTDLPLRASPSHIPSVVVLPTQQ	840
Qy	824	GYQHEYVDQPKMSEVAQMALEDQAATLEYKTIKEHLSSKSPNHGVNLVENLDSLPPKVPQ	883
Db	841	GYQHEYVDQPKMSEVAQMALEDQAATLEYKTIKEHLSSKSPNHGVNLVENLDSLPPKVPQ	900
Qy	884	REASLGPPGASLSQTGLSKRLEMHHSSSYGV DYKRSYPTNSLTRSHQATTLKRNTNSSN	943
Db	901	REASLGPPGASLSQTGLSKRLEMHHSSSYGV DYKRSYPTNSLTRSHQATTLKRNTNSSN	960
Qy	944	SSHLSRNQSFGRGDNPPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRT	1003
Db	961	SSHLSRNQSFGRGDNPPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRT	1020
Qy	1004	PSLKPDVPPKPSFAPLSTSMKPNDACT	1030
Db	1021	PSLKPDVPPKPSFAPLSTSMKPNDACT	1047

RESULT 6

US-10-449-548-14

; Sequence 14, Application US/10449548

```

; Publication No. US20040018977A1
; GENERAL INFORMATION:
; APPLICANT: Alvarez, Enrique
; APPLICANT: Anderson, David W.
; APPLICANT: Dhanabal, Mohanraj
; APPLICANT: Khramtsov, Nikolai V.
; APPLICANT: LaRochelle, William J.
; APPLICANT: Li, Li
; APPLICANT: Lichenstein, Henri
; APPLICANT: Ooi, Chean Eng
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: SEMAPHORIN-LIKE PROTEINS AND METHODS OF USING SAME
; FILE REFERENCE: 15966-540CIP2
; CURRENT APPLICATION NUMBER: US/10/449,548
; CURRENT FILING DATE: 2003-05-30
; PRIOR APPLICATION NUMBER: 09/520,781
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: 60/123,667
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: 60/234,082
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: 60/233,798
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 60/174,485
; PRIOR FILING DATE: 2000-01-04
; PRIOR APPLICATION NUMBER: 10/403,676
; PRIOR FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: 60/371,002
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/384,798
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/402,407
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 60/443,062
; PRIOR FILING DATE: 2003-01-28
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 14
; LENGTH: 1047
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-449-548-14

```

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Query Match          99.5%; Score 5422.5; DB 15; Length 1047;
Best Local Similarity 98.3%; Pred. No. 0;
Matches 1029; Conservative 0; Mismatches 1; Indels 17; Gaps 1;

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Qy      1 MRSEALLLYFTLLHFAGAGFPEDSEPISISHGNYTKQYPVFVGHKPGRNTTQRHRLDIQM 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MRSEALLLYFTLLHFAGAGFPEDSEPISISHCNYTKQYPVFVGHKPGRNTTQRHRLDIQM 60

Qy     61 IMIMNGTLYIAARDHIYTVDIDTSHTEEIYCSKKLTWKSQRQADVDTCRMKGKHKDECHNF 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 IMIMNGTLYIAARDHIYTVDIDTSHTEEIYCSKKLTWKSQRQADVDTCRMKGKHKDECHNF 120

```

Qy	121	IKVLLKKNDALFVCGTNAFNPSCRNYKMDTLEPFGDEFSGMARCPYDAKHANVALFADG	180
Db	121	IKVLLKKNDALFVCGTNAFNPSCRNYKMDTLEPFGDEFSGMARCPYDAKHANVALFADG	180
Qy	181	KLYSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLEKPYFVQAVDYGDIYFFFREIA	240
Db	181	KLYSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLEKPYFVQAVDYGDIYFFFREIA	240
Qy	241	VEYNTMGKVVFPRVAQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDSHFYFNILQAVT	300
Db	241	VEYNTMGKVVFPRVAQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDSHFYFNILQAVT	300
Qy	301	DVIRINGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVPDER	360
Db	301	DVIRINGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVPDER	360
Qy	361	VPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRL	420
Db	361	VPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRL	420
Qy	421	TKIAVDTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLNDSLFLEEMSVYNSEKCSYD	480
Db	421	TKIAVDTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLNDSLFLEEMSVYNSEKCSYD	480
Qy	481	GVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRCERHGKCKKTCIASRDPYCGWIKEGG	540
Db	481	GVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRCERHGKCKKTCIASRDPYCGWIKEGG	540
Qy	541	ACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALN-----GHSSSL	583
Db	541	ACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALNDISTPLPDNEMSYNTVYGHSSSL	600
Qy	584	PSTTTSDSTAQEGYESRGGMLDWKHLSDSPDSTDPLGAVSSHNHQDKKGVIRESYLKGH	643
Db	601	PSTTTSDSTAQEGYESRGGMLDWKHLSDSPDSTDPLGAVSSHNHQDKKGVIRESYLKGH	660
Qy	644	QLVPVTLIAIAVILAFVMGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRRGSMSSVT	703
Db	661	QLVPVTLIAIAVILAFVMGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRRGSMSSVT	720
Qy	704	KLSGLFGDTQSKDPKPEAILTPLMHNGKLATPGNTAKMLIKADQHHLDTALPTPESTPT	763
Db	721	KLSGLFGDTQSKDPKPEAILTPLMHNGKLATPGNTAKMLIKADQHHLDTALPTPESTPT	780
Qy	764	LQQKRKPSRGSREWERNQNLINACTKDMPPMGSPVIPTDLPLRASPSHIPSVVVLPI	823
Db	781	LQQKRKPSRGSREWERNQNLINACTKDMPPMGSPVIPTDLPLRASPSHIPSVVVLPI	840
Qy	824	GYQHEYVDQPKMSEVAQMALEDQAATLEYKTIKEHLSSKSPNHGVNLVENLDSLPPKVPQ	883
Db	841	GYQHEYVDQPKMSEVAQMALEDQAATLEYKTIKEHLSSKSPNHGVNLVENLDSLPPKVPQ	900
Qy	884	REASLGPPGASLSQTGLSKRLEMHHSSSYGVDYKRSYPTNSLTRSHQATTLKRNNNTSSN	943
Db	901	REASLGPPGASLSQTGLSKRLEMHHSSSYGVDYKRSYPTNSLTRSHQATTLKRNNNTSSN	960
Qy	944	SSHLSRNQSFGRGDNPPPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRT	1003

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          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      961 SSSLRNQSFGRGDNPPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRT 1020

Qy      1004 PSLKPDVPPKPSFAPLSTSMKPNDACT 1030
          ||||||||||||||||||||||||||||
Db      1021 PSLKPDVPPKPSFAPLSTSMKPNDACT 1047

```

RESULT 7

US-10-403-676-28

; Sequence 28, Application US/10403676

; Publication No. US20040029150A1

; GENERAL INFORMATION:

; APPLICANT: Alsobrook II, John

; APPLICANT: Anderson, David W.

; APPLICANT: Boldog, Ferenc L.

; APPLICANT: Burgess, Catherine E.

; APPLICANT: Casman, Stacie J.

; APPLICANT: Edinger, Shlomit R.

; APPLICANT: Gerlach, Valerie L.

; APPLICANT: Grosse, William M.

; APPLICANT: Guo, Xiaojia

; APPLICANT: Gusev, Vladimir Y.

; APPLICANT: Ji, Weizhen

; APPLICANT: LaRochelle, William J.

; APPLICANT: Lepley, Denise M.

; APPLICANT: Li, Li

; APPLICANT: Liu, Xiaohong

; APPLICANT: MacDougall, John R.

; APPLICANT: Malyankar, Uriel M.

; APPLICANT: Millet, Isabelle

; APPLICANT: Padigaru, Muralidhara

; APPLICANT: Patturajan, Meera

; APPLICANT: Peyman, John A.

; APPLICANT: Rastelli, Luca

; APPLICANT: Reiger, Daniel

; APPLICANT: Rothenberg, Mark E.

; APPLICANT: Shimkets, Richard A.

; APPLICANT: Stone, David J.

; APPLICANT: Taupier, Raymond J.

; APPLICANT: Vernet, Corine

; APPLICANT: Zerhusen, Bryan D.

; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME,
AND METHODS OF USE

; FILE REFERENCE: 21402-573B

; CURRENT APPLICATION NUMBER: US/10/403,676

; CURRENT FILING DATE: 2003-03-31

; PRIOR APPLICATION NUMBER: 60/123,667

; PRIOR FILING DATE: 1999-03-09

; PRIOR APPLICATION NUMBER: 09/520,781

; PRIOR FILING DATE: 2000-03-08

; PRIOR APPLICATION NUMBER: 09/957,187

; PRIOR FILING DATE: 2001-09-19

; PRIOR APPLICATION NUMBER: 60/371,002

; PRIOR FILING DATE: 2002-04-09

; PRIOR APPLICATION NUMBER: 60/127,352

; PRIOR FILING DATE: 1999-04-01

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; PRIOR APPLICATION NUMBER: 09/538,092
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 09/604,286
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 60/140,584
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 60/370,381
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/384,297
; PRIOR FILING DATE: 2002-05-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 179
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 28
; LENGTH: 1018
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-403-676-28

```

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Query Match          98.5%; Score 5368; DB 12; Length 1018;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1013; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

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Qy      17 GAGFPEDSEPISISHGNYTKQYPVFVGHKPGRNTTQRHRLDIQMIMIMNGTLYIAARDHI 76
      |:|
Db      2 GSGFPEDSEPISISHGNYTKQYPVFVGHKPGRNTTQRHRLDIQMIMIMNGTLYIAARDHI 61

Qy      77 YTVDIDTSHTEEIYCSKKLTWKSQRQADVDCRMKGKHKDECHNFIKVLLKKND DALFVCG 136
      |
Db      62 YTVDIDTSHTEEIYCSKKLTWKSQRQADVDCRMKGKHKDECHNFIKVLLKKND DALFVCG 121

Qy     137 TNAFNPSCRNYKMDTLEPGDEFSGMARCPYDAKHANVALFADGKLYSATVTDFLAIDAV 196
      |
Db     122 TNAFNPSCRNYKMDTLEPGDEFSGMARCPYDAKHANVALFADGKLYSATVTDFLAIDAV 181

Qy     197 IYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYFFFREIAVEYNTMGKVVFP RVAQ 256
      |
Db     182 IYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYFFFREIAVEYNTMGKVVFP RVAQ 241

Qy     257 VCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDSHFYFNILQAVTDVIRINGRDVVLATFS 316
      |
Db     242 VCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDSHFYFNILQAVTDVIRINGRDVVLATFS 301

Qy     317 TPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVPDERVPKPRPGCCAGSSSLE 376
      |
Db     302 TPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVPDERVPKPRPGCCAGSSSLE 361

Qy     377 RYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVR YRLTKIAVDTAAGPYQNHT 436
      |
Db     362 RYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVR YRLTKIAVDTAAGPYQNHT 421

Qy     437 VVFLGSEKGIILKFLARIGNSGFLNDSL FLEEMSVYNSEKCSYDGVEDKRIMGMQLDRAS 496
      |
Db     422 VVFLGSEKGIILKFLARIGNSGFLNDSL FLEEMSVYNSEKCSYDGVEDKRIMGMQLDRAS 481

Qy     497 SSLYVAFSTCVIKVPLGR CERH GKCKKTCIASRDPYCGWIKEGGACSHLSPNSRLTFEQD 556
      |

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Db	482	SSLYVAFSTCVIKVPLGR CERH GKCKKTCIASRDPYCGWIKEGGACSHLSPNSRLTFEQD	541
Qy	557	IERGNTDGLGDCHNSFVALNGHSSSLPSTTTSDSTAQEGYESRGGMLDWKHLLDSPDST	616
Db	542	IERGNTDGLGDCHNSFVALNGHSSSLPSTTTSDSTAQEGYESRGGMLDWKHLLDSPDST	601
Qy	617	DPLGAVSSHNHQDKKGVIRESYLKGHDLVPVTL LAIAVILAFVMGAVFSGITVYCVCDH	676
Db	602	DPLGAVSSHNHQDKKGVIRESYLKGHDLVPVTL LAIAVILAFVMGAVFSGITVYCVCDH	661
Qy	677	RRKDVAVVQRKEKELTHSRGSMSSVTKL SGLFGDTQSKDPKPEAILTPLMHNGKLATPG	736
Db	662	RRKDVAVVQRKEKELTHSRGSMSSVTKL SGLFGDTQSKDPKPEAILTPLMHNGKLATPG	721
Qy	737	NTAKMLIKADQHHLDTALPTPESTPTLQQKRKPSRGSREWERNQN LINACTKDMPPMGS	796
Db	722	NTAKMLIKADQHHLDTALPTPESTPTLQQKRKPSRGSREWERNQN LINACTKDMPPMGS	781
Qy	797	PVIPTDLPLRASPSHIPSVVVLPI TQQGYQHEYVDQPKMSEVAQMALEDQAATLEYKTIK	856
Db	782	PVIPTDLPLRASPSHIPSVVVLPI TQQGYQHEYVDQPKMSEVAQMALEDQAATLEYKTIK	841
Qy	857	EHLSSKSPNHGVNLVENLDSLPPKVPQREASLGPPGASLSQTGLSKRLEMHHSSSYGVDY	916
Db	842	EHLSSKSPNHGVNLVENLDSLPPKVPQREASLGPPGASLSQTGLSKRLEMHHSSSYGVDY	901
Qy	917	KRSYPTNSLTRSHQATTLKRNTNSSNSSHL SRNQSFGRGDNPPAPQRVDSIQVHSSQP	976
Db	902	KRSYPTNSLTRSHQATTLKRNTNSSNSSHL SRNQSFGRGDNPPAPQRVDSIQVHSSQP	961
Qy	977	SGQAVTVSRQPSLNAYNSLTRSGLKRTPSLKPDPVPPKPSFAPLSTSMKPNDACT	1030
Db	962	SGQAVTVSRQPSLNAYNSLTRSGLKRTPSLKPDPVPPKPSFAPLSTSMKPNDACT	1015

RESULT 8

US-10-449-548-28

; Sequence 28, Application US/10449548

; Publication No. US20040018977A1

; GENERAL INFORMATION:

; APPLICANT: Alvarez, Enrique

; APPLICANT: Anderson, David W.

; APPLICANT: Dhanabal, Mohanraj

; APPLICANT: Khramtsov, Nikolai V.

; APPLICANT: LaRochelle, William J.

; APPLICANT: Li, Li

; APPLICANT: Lichenstein, Henri

; APPLICANT: Ooi, Chean Eng

; APPLICANT: Padigar, Muralidhara

; APPLICANT: Shimkets, Richard A.

; APPLICANT: Zhong, Mei

; TITLE OF INVENTION: SEMAPHORIN-LIKE PROTEINS AND METHODS OF USING SAME

; FILE REFERENCE: 15966-540CIP2

; CURRENT APPLICATION NUMBER: US/10/449,548

; CURRENT FILING DATE: 2003-05-30

; PRIOR APPLICATION NUMBER: 09/520,781

; PRIOR FILING DATE: 2000-03-03

```
; PRIOR APPLICATION NUMBER: 60/123,667
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: 60/234,082
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: 60/233,798
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 60/174,485
; PRIOR FILING DATE: 2000-01-04
; PRIOR APPLICATION NUMBER: 10/403,676
; PRIOR FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: 60/371,002
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/384,798
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/402,407
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 60/443,062
; PRIOR FILING DATE: 2003-01-28
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 28
; LENGTH: 1018
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-449-548-28
```

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Query Match          98.5%; Score 5368; DB 15; Length 1018;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1013; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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Qy      17 GAGFPEDSEPISISHGNYTKQYPVFVGHKPGRNTTQRHRLDIQMIMNGTLYIAARDHI 76
      |:|||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2 GSGFPEDSEPISISHGNYTKQYPVFVGHKPGRNTTQRHRLDIQMIMNGTLYIAARDHI 61

Qy      77 YTVDIDTSHTEEIYCSKKLTWKSQRQADVDTCRMKGKHKDECHNFIKVLLKKND DALFVCG 136
      |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      62 YTVDIDTSHTEEIYCSKKLTWKSQRQADVDTCRMKGKHKDECHNFIKVLLKKND DALFVCG 121

Qy     137 TNAFNPSCRNYKMDTLEPGDEFSGMARCPYDAKHANVALFADGKLYSATVTDFLAIDAV 196
      |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     122 TNAFNPSCRNYKMDTLEPGDEFSGMARCPYDAKHANVALFADGKLYSATVTDFLAIDAV 181

Qy     197 IYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYFFFREIAVEYNTMGKVVFPRVAQ 256
      |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     182 IYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYFFFREIAVEYNTMGKVVFPRVAQ 241

Qy     257 VCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDSHFYFNILQAVTDVIRINGRDVVLATFS 316
      |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     242 VCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDSHFYFNILQAVTDVIRINGRDVVLATFS 301

Qy     317 TPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTFVPDERVPKPRPGCCAGSSSLE 376
      |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     302 TPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTFVPDERVPKPRPGCCAGSSSLE 361

Qy     377 RYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRLTKIAVDTAAGPYQNHT 436
      |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     362 RYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRLTKIAVDTAAGPYQNHT 421
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Qy	437	VVFLGSEKGIILKFLARIGNSGFLNDSLFLEEMSVYNSEKCSYDGVEDKRIMGMLDRAS	496
Db	422	VVFLGSEKGIILKFLARIGNSGFLNDSLFLEEMSVYNSEKCSYDGVEDKRIMGMLDRAS	481
Qy	497	SSLYVAFSTCVIKVPLGRCERHGKCKKTCIASRDPYCGWKEGGACSHLSPNSRLTFEQD	556
Db	482	SSLYVAFSTCVIKVPLGRCERHGKCKKTCIASRDPYCGWKEGGACSHLSPNSRLTFEQD	541
Qy	557	IERGNTDGLGDCHNSFVALNGHSSSLPSTTTSDSTAQEGYESRGGMLDWKHLDSPDST	616
Db	542	IERGNTDGLGDCHNSFVALNGHSSSLPSTTTSDSTAQEGYESRGGMLDWKHLDSPDST	601
Qy	617	DPLGAVSSHNHQDKKGVIRESYLKGHDQLVPVTLIAIVILAFVMGAVFSGITVYCVCDH	676
Db	602	DPLGAVSSHNHQDKKGVIRESYLKGHDQLVPVTLIAIVILAFVMGAVFSGITVYCVCDH	661
Qy	677	RRKDVAVVQRKEKELTHSRGSMSSVTKL SGLFGDTQSKDPKPEAILTPLMHNGKLATPG	736
Db	662	RRKDVAVVQRKEKELTHSRGSMSSVTKL SGLFGDTQSKDPKPEAILTPLMHNGKLATPG	721
Qy	737	NTAKMLIKADQHHLDTALPTPESTPTLQQKRKPSRGSREWERNQNLINACTKDMPPMGS	796
Db	722	NTAKMLIKADQHHLDTALPTPESTPTLQQKRKPSRGSREWERNQNLINACTKDMPPMGS	781
Qy	797	PVIPTDLPLRASPSHIPSVVVLPIITQQGYQHEYVDQPKMSEVAQMALEDQAATLEYKTIK	856
Db	782	PVIPTDLPLRASPSHIPSVVVLPIITQQGYQHEYVDQPKMSEVAQMALEDQAATLEYKTIK	841
Qy	857	EHLSSKSPNHGVNLVENLDSLPPKVPQREASLGPPGASLSQTGLSKRLEMHHSSSYGVDY	916
Db	842	EHLSSKSPNHGVNLVENLDSLPPKVPQREASLGPPGASLSQTGLSKRLEMHHSSSYGVDY	901
Qy	917	KRSYPTNSLTRSHQATTLKRNTNSSNSSHL SRNQSFGRGDNPPPPAPQRVDSIQVHSSQP	976
Db	902	KRSYPTNSLTRSHQATTLKRNTNSSNSSHL SRNQSFGRGDNPPPPAPQRVDSIQVHSSQP	961
Qy	977	SGQAVTVSRQPSLNAYNSLTRSGLKRTPSLKPDVPPKPSFAPLSTSMKPNDACT	1030
Db	962	SGQAVTVSRQPSLNAYNSLTRSGLKRTPSLKPDVPPKPSFAPLSTSMKPNDACT	1015

RESULT 9

US-10-403-676-18

; Sequence 18, Application US/10403676

; Publication No. US20040029150A1

; GENERAL INFORMATION:

; APPLICANT: Alsobrook II, John

; APPLICANT: Anderson, David W.

; APPLICANT: Boldog, Ferenc L.

; APPLICANT: Burgess, Catherine E.

; APPLICANT: Casman, Stacie J.

; APPLICANT: Edinger, Shlomit R.

; APPLICANT: Gerlach, Valerie L.

; APPLICANT: Grosse, William M.

; APPLICANT: Guo, Xiaojia

; APPLICANT: Gusev, Vladimir Y.

```

; APPLICANT: Ji, Weizhen
; APPLICANT: LaRochelle, William J.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Li, Li
; APPLICANT: Liu, Xiaohong
; APPLICANT: MacDougall, John R.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Millet, Isabelle
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Patturajan, Meera
; APPLICANT: Peyman, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Reiger, Daniel
; APPLICANT: Rothenberg, Mark E.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Stone, David J.
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Vernet, Corine
; APPLICANT: Zerhusen, Bryan D.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME,
AND METHODS OF USE
; FILE REFERENCE: 21402-573B
; CURRENT APPLICATION NUMBER: US/10/403,676
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: 60/123,667
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: 09/520,781
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 09/957,187
; PRIOR FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/371,002
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 09/538,092
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 09/604,286
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 60/140,584
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 60/370,381
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/384,297
; PRIOR FILING DATE: 2002-05-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 179
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 18
; LENGTH: 1035
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-403-676-18

```

```

Query Match          98.2%; Score 5349.5; DB 12; Length 1035;
Best Local Similarity 98.3%; Pred. No. 0;
Matches 1013; Conservative 1; Mismatches 0; Indels 17; Gaps 1;

```

Qy	17	GAGFPEDSEPI SISHGNYTKQYPVFVGHKPGRNTTQRHRLDIQMIMIMNGTLYIAARDHI	76
		:	
Db	2	GSGFPEDSEPI SISHGNYTKQYPVFVGHKPGRNTTQRHRLDIQMIMIMNGTLYIAARDHI	61
Qy	77	YTVDIDTSHTEEIYCSKKLTWKSQRQADVDTCRMKGKHKDECHNFIKVLLKKND DALFVCG	136
Db	62	YTVDIDTSHTEEIYCSKKLTWKSQRQADVDTCRMKGKHKDECHNFIKVLLKKND DALFVCG	121
Qy	137	TNAFNPSCRNYKMDTLEPFGDEFSGMARCPYDAKHANVALFADGKLYSATVTD FLAIDAV	196
Db	122	TNAFNPSCRNYKMDTLEPFGDEFSGMARCPYDAKHANVALFADGKLYSATVTD FLAIDAV	181
Qy	197	IYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYFFFREIAVEYNTMGKVVFPRVAQ	256
Db	182	IYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYFFFREIAVEYNTMGKVVFPRVAQ	241
Qy	257	VCKNDMGGSQRVLEKQWTSFLKARLNC SVPGDSHFYFNILQAVTDVIRINGRDVVLATFS	316
Db	242	VCKNDMGGSQRVLEKQWTSFLKARLNC SVPGDSHFYFNILQAVTDVIRINGRDVVLATFS	301
Qy	317	TPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVPDERVPKPRPGCCAGSSSLE	376
Db	302	TPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVPDERVPKPRPGCCAGSSSLE	361
Qy	377	RYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRLTKIAVDTAAGPYQNHT	436
Db	362	RYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRLTKIAVDTAAGPYQNHT	421
Qy	437	VVFLGSEKGIILKFLARIGNSGFLNDSL FLEEMSVYNSEKCSYDGVEDKRIMGMLDRAS	496
Db	422	VVFLGSEKGIILKFLARIGNSGFLNDSL FLEEMSVYNSEKCSYDGVEDKRIMGMLDRAS	481
Qy	497	SSLYVAFSTCVIKVPLGRCERHGKCKKTCIASRDPYCGWIEGGACSHLSPNSRLTFEQD	556
Db	482	SSLYVAFSTCVIKVPLGRCERHGKCKKTCIASRDPYCGWIEGGACSHLSPNSRLTFEQD	541
Qy	557	IERGNTDGLGDCHNSFVALN-----GHSSSLLPSTTTSDSTAQEGYES	599
Db	542	IERGNTDGLGDCHNSFVALNDISTPLPDNEMSYNTVYGHSSSLLPSTTTSDSTAQEGYES	601
Qy	600	RGGMLDWKHLLDSPDSTDPLGAVSSH NHQDKKGVIRESYLKGHDLVPVTL LAIAVILAF	659
Db	602	RGGMLDWKHLLDSPDSTDPLGAVSSH NHQDKKGVIRESYLKGHDLVPVTL LAIAVILAF	661
Qy	660	VMGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRRGSMSSVTKLSGLFGDTQSKDPKP	719
Db	662	VMGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRRGSMSSVTKLSGLFGDTQSKDPKP	721
Qy	720	EAILTPLMHNGKLATPGNTAKMLIKADQHHLDTALPTPESTPTLQQKRKPSRGSREWER	779
Db	722	EAILTPLMHNGKLATPGNTAKMLIKADQHHLDTALPTPESTPTLQQKRKPSRGSREWER	781
Qy	780	NQNLINACTKDMPPMGSPVIPTDLPLRASPSHIPSVVVLPI TQQGYQHEYVDQPKMSEVA	839
Db	782	NQNLINACTKDMPPMGSPVIPTDLPLRASPSHIPSVVVLPI TQQGYQHEYVDQPKMSEVA	841
Qy	840	QMALEDQAATLEYKTIKEHLSSKSPNHGVNLVENLDSLPPKVPQREASLGPPGASLSQTG	899

Db	842	QMALEDQAATLEYKTIKEHLSSKSPNHGVNLVENLDSLPPKVPQREASLGPPGASLSQTG	901
Qy	900	LSKRLEMHHSSSYGVDYKRSYPTNSLTRSHQATTLKRNTNSSNSSHLSRNQSFGRGDNF	959
Db	902	LSKRLEMHHSSSYGVDYKRSYPTNSLTRSHQATTLKRNTNSSNSSHLSRNQSFGRGDNF	961
Qy	960	PPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRTPSLKPDPVPPKPSFAPL	1019
Db	962	PPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRTPSLKPDPVPPKPSFAPL	1021
Qy	1020	STSMKPNDACT	1030
Db	1022	STSMKPNDACT	1032

RESULT 10

US-10-449-548-18

; Sequence 18, Application US/10449548

; Publication No. US20040018977A1

; GENERAL INFORMATION:

; APPLICANT: Alvarez, Enrique

; APPLICANT: Anderson, David W.

; APPLICANT: Dhanabal, Mohanraj

; APPLICANT: Khramtsov, Nikolai V.

; APPLICANT: LaRochelle, William J.

; APPLICANT: Li, Li

; APPLICANT: Lichenstein, Henri

; APPLICANT: Ooi, Chean Eng

; APPLICANT: Padigar, Muralidhara

; APPLICANT: Shimkets, Richard A.

; APPLICANT: Zhong, Mei

; TITLE OF INVENTION: SEMAPHORIN-LIKE PROTEINS AND METHODS OF USING SAME

; FILE REFERENCE: 15966-540CIP2

; CURRENT APPLICATION NUMBER: US/10/449,548

; CURRENT FILING DATE: 2003-05-30

; PRIOR APPLICATION NUMBER: 09/520,781

; PRIOR FILING DATE: 2000-03-03

; PRIOR APPLICATION NUMBER: 60/123,667

; PRIOR FILING DATE: 1999-03-09

; PRIOR APPLICATION NUMBER: 60/234,082

; PRIOR FILING DATE: 2000-09-20

; PRIOR APPLICATION NUMBER: 60/233,798

; PRIOR FILING DATE: 2000-09-19

; PRIOR APPLICATION NUMBER: 60/174,485

; PRIOR FILING DATE: 2000-01-04

; PRIOR APPLICATION NUMBER: 10/403,676

; PRIOR FILING DATE: 2003-03-31

; PRIOR APPLICATION NUMBER: 60/371,002

; PRIOR FILING DATE: 2002-04-09

; PRIOR APPLICATION NUMBER: 60/384,798

; PRIOR FILING DATE: 2002-05-30

; PRIOR APPLICATION NUMBER: 60/402,407

; PRIOR FILING DATE: 2002-08-09

; PRIOR APPLICATION NUMBER: 60/443,062

; PRIOR FILING DATE: 2003-01-28

; NUMBER OF SEQ ID NOS: 58

Db	662	VMGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRRGSMSSVTKLSGLFGDTQSKDPKP	721
Qy	720	EAILTPLMHNGKLATPGNTAKMLIKADQHHLDTALPTPESTPTLQQKRKPSRGSREWER	779
Db	722	EAILTPLMHNGKLATPGNTAKMLIKADQHHLDTALPTPESTPTLQQKRKPSRGSREWER	781
Qy	780	NQNLINACTKDMPPMGSPVIPTDLPLRASPSHIPSVVVLPIITQQGYQHEYVDQPKMSEVA	839
Db	782	NQNLINACTKDMPPMGSPVIPTDLPLRASPSHIPSVVVLPIITQQGYQHEYVDQPKMSEVA	841
Qy	840	QMALEDQAATLEYKTIKEHLSSKSPNHGVNLVENLDSLPPKVPQREASLGPPGASLSQTG	899
Db	842	QMALEDQAATLEYKTIKEHLSSKSPNHGVNLVENLDSLPPKVPQREASLGPPGASLSQTG	901
Qy	900	LSKRLEMHHSSSYGVDYKRSYPTNSLTRSHQATTLKRNNNTSSNSSHLNRNQSFGRGDNP	959
Db	902	LSKRLEMHHSSSYGVDYKRSYPTNSLTRSHQATTLKRNNNTSSNSSHLNRNQSFGRGDNP	961
Qy	960	PPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRTPSLKPDPVPPKPSFAPL	1019
Db	962	PPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRTPSLKPDPVPPKPSFAPL	1021
Qy	1020	STSMKPNDACT	1030
Db	1022	STSMKPNDACT	1032

RESULT 11

US-10-403-676-20

; Sequence 20, Application US/10403676

; Publication No. US20040029150A1

; GENERAL INFORMATION:

; APPLICANT: Alsobrook II, John
; APPLICANT: Anderson, David W.
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Grosse, William M.
; APPLICANT: Guo, Xiaojia
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Ji, Weizhen
; APPLICANT: LaRochelle, William J.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Li, Li
; APPLICANT: Liu, Xiaohong
; APPLICANT: MacDougall, John R.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Millet, Isabelle
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Patturajan, Meera
; APPLICANT: Peyman, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Reiger, Daniel
; APPLICANT: Rothenberg, Mark E.
; APPLICANT: Shimkets, Richard A.


```

; APPLICANT: Stone, David J.
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Vernet, Corine
; APPLICANT: Zerhusen, Bryan D.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME,
AND METHODS OF USE
; FILE REFERENCE: 21402-573B
; CURRENT APPLICATION NUMBER: US/10/403,676
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: 60/123,667
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: 09/520,781
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 09/957,187
; PRIOR FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/371,002
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 09/538,092
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 09/604,286
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 60/140,584
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 60/370,381
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/384,297
; PRIOR FILING DATE: 2002-05-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 179
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 20
; LENGTH: 998
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-403-676-20

```

```

Query Match          94.2%; Score 5134.5; DB 12; Length 998;
Best Local Similarity 98.3%; Pred. No. 0;
Matches 975; Conservative 0; Mismatches 0; Indels 17; Gaps 1;

```

```

Qy      56 LDIQMIMIMNGTLYIAARDHIYTVDIDTSHTEEIYCSKKLTWKSQRQADVDTCRMKGKHKD 115
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4 LDIQMIMIMNGTLYIAARDHIYTVDIDTSHTEEIYCSKKLTWKSQRQADVDTCRMKGKHKD 63

Qy     116 ECHNFIKVLLKKNDALFVCGTNAFNPSCRNYKMDTLEPGDEFSGMARCPYDAKHANVA 175
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      64 ECHNFIKVLLKKNDALFVCGTNAFNPSCRNYKMDTLEPGDEFSGMARCPYDAKHANVA 123

Qy     176 LFADGKLYSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYFF 235
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     124 LFADGKLYSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYFF 183

Qy     236 FREIAVEYNTMGKVVFPRVAQVCKNDMGGSQRVLEKQWTSFLKARLNCSPVGDShFYFNI 295
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     184 FREIAVEYNTMGKVVFPRVAQVCKNDMGGSQRVLEKQWTSFLKARLNCSPVGDShFYFNI 243

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Qy	296	LQAVTDVIRINGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTP	355
Db	244	LQAVTDVIRINGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTP	303
Qy	356	VPDERVPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTM	415
Db	304	VPDERVPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTM	363
Qy	416	VRYRLTKIAVDTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLNDSLFLEEMSVYNSE	475
Db	364	VRYRLTKIAVDTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLNDSLFLEEMSVYNSE	423
Qy	476	KCSYDGVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRGERHGKCKKTCIASRDPYCGW	535
Db	424	KCSYDGVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRGERHGKCKKTCIASRDPYCGW	483
Qy	536	IKEGGACSHLSPNSRLTFEQDIERGNTDGLGDCCHNSFVALN-----GH	578
Db	484	IKEGGACSHLSPNSRLTFEQDIERGNTDGLGDCCHNSFVALNDISTPLPDNEMSYNTVYGH	543
Qy	579	SSSLPSTTTSDSTAQEGYESRGGMLDWKHLLDSPDSTDPLGAVSSHNDKKGVIRESY	638
Db	544	SSSLPSTTTSDSTAQEGYESRGGMLDWKHLLDSPDSTDPLGAVSSHNDKKGVIRESY	603
Qy	639	LKGHDQLVPVTLIAIAVILAFVMGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRGS	698
Db	604	LKGHDQLVPVTLIAIAVILAFVMGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRGS	663
Qy	699	MSSVTKLSGLFGDTQSKDPKPEAILTPLMHNGKLATPGNTAKMLIKADQHHLDTALPTP	758
Db	664	MSSVTKLSGLFGDTQSKDPKPEAILTPLMHNGKLATPGNTAKMLIKADQHHLDTALPTP	723
Qy	759	ESTPTLQQKRKPSRGSREWERNQNLINACTKDMPPMGSPVIPTDLPLRASPSHIPSVVVL	818
Db	724	ESTPTLQQKRKPSRGSREWERNQNLINACTKDMPPMGSPVIPTDLPLRASPSHIPSVVVL	783
Qy	819	PITQQGYQHEYVDQPKMSEVAQMALEDQAATLEYKTIKEHLSSKSPNHGVNLVENLDSLP	878
Db	784	PITQQGYQHEYVDQPKMSEVAQMALEDQAATLEYKTIKEHLSSKSPNHGVNLVENLDSLP	843
Qy	879	PKVPQREASLGPPGASLSQTGLSKRLEMHHSSSYGVDYKRSYPTNSLTRSHQATTLKRNN	938
Db	844	PKVPQREASLGPPGASLSQTGLSKRLEMHHSSSYGVDYKRSYPTNSLTRSHQATTLKRNN	903
Qy	939	TNSSNSSHLNRNQSFGRGDNPPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRS	998
Db	904	TNSSNSSHLNRNQSFGRGDNPPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRS	963
Qy	999	GLKRTPSLKPDPVPPKPSFAPLSTSMKPNDACT	1030
Db	964	GLKRTPSLKPDPVPPKPSFAPLSTSMKPNDACT	995

RESULT 12

US-10-449-548-20

; Sequence 20, Application US/10449548

```

; Publication No. US20040018977A1
; GENERAL INFORMATION:
; APPLICANT: Alvarez, Enrique
; APPLICANT: Anderson, David W.
; APPLICANT: Dhanabal, Mohanraj
; APPLICANT: Khramtsov, Nikolai V.
; APPLICANT: LaRochelle, William J.
; APPLICANT: Li, Li
; APPLICANT: Lichenstein, Henri
; APPLICANT: Ooi, Chean Eng
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: SEMAPHORIN-LIKE PROTEINS AND METHODS OF USING SAME
; FILE REFERENCE: 15966-540CIP2
; CURRENT APPLICATION NUMBER: US/10/449,548
; CURRENT FILING DATE: 2003-05-30
; PRIOR APPLICATION NUMBER: 09/520,781
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: 60/123,667
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: 60/234,082
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: 60/233,798
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 60/174,485
; PRIOR FILING DATE: 2000-01-04
; PRIOR APPLICATION NUMBER: 10/403,676
; PRIOR FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: 60/371,002
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/384,798
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/402,407
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 60/443,062
; PRIOR FILING DATE: 2003-01-28
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 20
; LENGTH: 998
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-449-548-20

```

```

Query Match          94.2%; Score 5134.5; DB 15; Length 998;
Best Local Similarity 98.3%; Pred. No. 0;
Matches 975; Conservative 0; Mismatches 0; Indels 17; Gaps 1;

```

```

Qy      56 LDIQMIMIMNGTLYIAARDHIYTVDIDTSHTEEIYCSKKLTWKSQRQADVDTCRMKGKHKD 115
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4  LDIQMIMIMNGTLYIAARDHIYTVDIDTSHTEEIYCSKKLTWKSQRQADVDTCRMKGKHKD 63

Qy     116 ECHNFIKVLLKKNDDALFVCGTNAFNPSCRNYKMDTLEPFGDEFSGMARCPYDAKHANVA 175
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     64  ECHNFIKVLLKKNDDALFVCGTNAFNPSCRNYKMDTLEPFGDEFSGMARCPYDAKHANVA 123

```

Qy	176	LFADGKLYSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYFF	235
Db	124	LFADGKLYSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYFF	183
Qy	236	FREIAVEYNTMGKVVFPRAVQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDSHFYFNI	295
Db	184	FREIAVEYNTMGKVVFPRAVQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDSHFYFNI	243
Qy	296	LQAVTDVIRINGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTP	355
Db	244	LQAVTDVIRINGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTP	303
Qy	356	VPDERVPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTM	415
Db	304	VPDERVPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTM	363
Qy	416	VRYRLTKIAVDTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLNDSLFLEEMSVYNSE	475
Db	364	VRYRLTKIAVDTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLNDSLFLEEMSVYNSE	423
Qy	476	KCSYDGVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRCERHGKCKKTCIASRDPYCGW	535
Db	424	KCSYDGVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRCERHGKCKKTCIASRDPYCGW	483
Qy	536	IKEGGACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALN-----GH	578
Db	484	IKEGGACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALNDISTPLPDNEMSINTVYGH	543
Qy	579	SSSLPSTTTSDSTAQEGYESRGGMLDWKHLSDPDSTDPLGAVSSHNDKKGVIRESY	638
Db	544	SSSLPSTTTSDSTAQEGYESRGGMLDWKHLSDPDSTDPLGAVSSHNDKKGVIRESY	603
Qy	639	LKGHDQLVPVTLIAIAVILAFVMGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRGS	698
Db	604	LKGHDQLVPVTLIAIAVILAFVMGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRGS	663
Qy	699	MSSVTKLSGLFGDTQSKDPKPEAILTPLMHNGKLATPGNTAKMLIKADQHHLDTALPTP	758
Db	664	MSSVTKLSGLFGDTQSKDPKPEAILTPLMHNGKLATPGNTAKMLIKADQHHLDTALPTP	723
Qy	759	ESTPTLQQKRKPSRGSREWERNQNINACTKDMPPMGSPVIPTDLPLRASPSHIPSVVVL	818
Db	724	ESTPTLQQKRKPSRGSREWERNQNINACTKDMPPMGSPVIPTDLPLRASPSHIPSVVVL	783
Qy	819	PITQQGYQHEYVDQPKMSEVAQMALEDQAATLEYKTIKEHLSSKSPNHGVNLVENLDSLP	878
Db	784	PITQQGYQHEYVDQPKMSEVAQMALEDQAATLEYKTIKEHLSSKSPNHGVNLVENLDSLP	843
Qy	879	PKVPQREASLGPPGASLSQTGLSKRLEMHHSSSYGVYDKRSYPTNSLTRSHQATTLKRNN	938
Db	844	PKVPQREASLGPPGASLSQTGLSKRLEMHHSSSYGVYDKRSYPTNSLTRSHQATTLKRNN	903
Qy	939	TNSSNSSHLNRNQSFRGDNPPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRS	998
Db	904	TNSSNSSHLNRNQSFRGDNPPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRS	963
Qy	999	GLKRTPSLKPDPVPPKPSFAPLSTSMKPNDACT	1030

RESULT 13

US-10-403-676-30

; Sequence 30, Application US/10403676

; Publication No. US20040029150A1

; GENERAL INFORMATION:

; APPLICANT: Alsobrook II, John

; APPLICANT: Anderson, David W.

; APPLICANT: Boldog, Ferenc L.

; APPLICANT: Burgess, Catherine E.

; APPLICANT: Casman, Stacie J.

; APPLICANT: Edinger, Shlomit R.

; APPLICANT: Gerlach, Valerie L.

; APPLICANT: Grosse, William M.

; APPLICANT: Guo, Xiaojia

; APPLICANT: Gusev, Vladimir Y.

; APPLICANT: Ji, Weizhen

; APPLICANT: LaRochelle, William J.

; APPLICANT: Lepley, Denise M.

; APPLICANT: Li, Li

; APPLICANT: Liu, Xiaohong

; APPLICANT: MacDougall, John R.

; APPLICANT: Malyankar, Uriel M.

; APPLICANT: Millet, Isabelle

; APPLICANT: Padigar, Muralidhara

; APPLICANT: Patturajan, Meera

; APPLICANT: Peyman, John A.

; APPLICANT: Rastelli, Luca

; APPLICANT: Reiger, Daniel

; APPLICANT: Rothenberg, Mark E.

; APPLICANT: Shimkets, Richard A.

; APPLICANT: Stone, David J.

; APPLICANT: Taupier, Raymond J.

; APPLICANT: Vernet, Corine

; APPLICANT: Zerhusen, Bryan D.

; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME,
AND METHODS OF USE

; FILE REFERENCE: 21402-573B

; CURRENT APPLICATION NUMBER: US/10/403,676

; CURRENT FILING DATE: 2003-03-31

; PRIOR APPLICATION NUMBER: 60/123,667

; PRIOR FILING DATE: 1999-03-09

; PRIOR APPLICATION NUMBER: 09/520,781

; PRIOR FILING DATE: 2000-03-08

; PRIOR APPLICATION NUMBER: 09/957,187

; PRIOR FILING DATE: 2001-09-19

; PRIOR APPLICATION NUMBER: 60/371,002

; PRIOR FILING DATE: 2002-04-09

; PRIOR APPLICATION NUMBER: 60/127,352

; PRIOR FILING DATE: 1999-04-01

; PRIOR APPLICATION NUMBER: 09/538,092

; PRIOR FILING DATE: 2000-03-29

; PRIOR APPLICATION NUMBER: 09/604,286

; PRIOR FILING DATE: 2000-06-22

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; PRIOR APPLICATION NUMBER: 60/140,584
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 60/370,381
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/384,297
; PRIOR FILING DATE: 2002-05-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 179
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 30
; LENGTH: 981
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-403-676-30
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Query Match          93.8%; Score 5113.5; DB 12; Length 981;
Best Local Similarity 94.6%; Pred. No. 0;
Matches 974; Conservative 0; Mismatches 1; Indels 55; Gaps 1;
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Qy      1 MRSEALLLYFTLLHFAGAGFPEDSEPI SISHGNYTKQYPVFGHKPGRNTTQRHRLDIQM 60
        |
Db      4 MRSEALLLYFTLLHFAGAGFPEDSEPI SISHGNYTKQYPVFGHKPGRNTTQRHRLDIQM 63

Qy     61 IMIMNGTLYIAARDHIYTVDIDTSHTEEEIYCSKKLTWKSQRQADVDTCRMKGKHKDECHNF 120
        |
Db     64 IMIMNGTLYIAARDHIYTVDIDTSHTEEEIYCSKKLTWKSQRQADVDTCRMKGKHKDECHNF 123

Qy    121 IKVLLKKND DALFVCGTNAFNPSCRNYKMDTLEPF GDEFSGMARCPYDAKHANVALFADG 180
        |
Db    124 IKVLLKKND DALFVCGTNAFNPSCRNYKMDTLEPF GDEFSGMARCPYDAKHANVALFADG 183

Qy    181 KLYSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDYIYFFFREIA 240
        |
Db    184 KLYSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDYIYFFFREIA 243

Qy    241 VEYNTMGKVVFPRVAQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDSHFYFNILQAVT 300
        |
Db    244 VEYNTMGKVVFPRVAQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDSHFYFNILQAVT 303

Qy    301 DVIRINGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVPDER 360
        |
Db    304 DVIRIKGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVPDER 363

Qy    361 VPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVR YRL 420
        |
Db    364 VPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVR YRL 423

Qy    421 TKIAVDTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLNDSLFLEEMSVYNSEKCSYD 480
        |
Db    424 TKIAVDTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLNDSLFLEEMSVYNSEKCSYD 483

Qy    481 GVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGR CERHKGCKKTCIASRDPYCGWIKEGG 540
        |
Db    484 GVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGR CERHKGCKKTCIASRDPYCGWIKEGG 543

Qy    541 ACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALNGHSSSLPSTTTSDSTAQEGYESR 600
        |
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Db	544	ACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALN-----	579
Qy	601	GGMLDWKHLLDSPDSTDPLGAVSSHNHQQDKKGVIRESYLKGHDLVPVTTLLAIAVILAFV	660
Db	580	-----GVIRESYLKGHDLVPVTTLLAIAVILAFV	608
Qy	661	MGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRRGSMSSVTKLSGLFGDTQSKDPKPE	720
Db	609	MGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRRGSMSSVTKLSGLFGDTQSKDPKPE	668
Qy	721	AILTPLMHNGKLATPGNTAKMLIKADQHHLDLTALPTPESTPTLQQKRKPSRGSREWERN	780
Db	669	AILTPLMHNGKLATPGNTAKMLIKADQHHLDLTALPTPESTPTLQQKRKPSRGSREWERN	728
Qy	781	QNLINACTKDMPPMGSPVIPTDLPLRASPSHIPSVVVLPIITQQGYQHEYVDQPKMSEVAQ	840
Db	729	QNLINACTKDMPPMGSPVIPTDLPLRASPSHIPSVVVLPIITQQGYQHEYVDQPKMSEVAQ	788
Qy	841	MALEDQAATLEYKTIKEHLSSKSPNHGVNLVENLDSLPPKVPQREASLGPPGASLSQTGL	900
Db	789	MALEDQAATLEYKTIKEHLSSKSPNHGVNLVENLDSLPPKVPQREASLGPPGASLSQTGL	848
Qy	901	SKRLEMHHSSSYGVVDYKRSYPTNSLTRSHQATTLKRNTNSSNSSHLSRNQSFGRGDNPP	960
Db	849	SKRLEMHHSSSYGVVDYKRSYPTNSLTRSHQATTLKRNTNSSNSSHLSRNQSFGRGDNPP	908
Qy	961	PAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRTPSLKPDVPPKPSFAPLS	1020
Db	909	PAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRTPSLKPDVPPKPSFAPLS	968
Qy	1021	TSMKPNDACT	1030
Db	969	TSMKPNDACT	978

RESULT 14

US-10-449-548-30

; Sequence 30, Application US/10449548

; Publication No. US20040018977A1

; GENERAL INFORMATION:

; APPLICANT: Alvarez, Enrique

; APPLICANT: Anderson, David W.

; APPLICANT: Dhanabal, Mohanraj

; APPLICANT: Khramtsov, Nikolai V.

; APPLICANT: LaRochelle, William J.

; APPLICANT: Li, Li

; APPLICANT: Lichenstein, Henri

; APPLICANT: Ooi, Chean Eng

; APPLICANT: Padigar, Muralidhara

; APPLICANT: Shimkets, Richard A.

; APPLICANT: Zhong, Mei

; TITLE OF INVENTION: SEMAPHORIN-LIKE PROTEINS AND METHODS OF USING SAME

; FILE REFERENCE: 15966-540CIP2

; CURRENT APPLICATION NUMBER: US/10/449,548

; CURRENT FILING DATE: 2003-05-30

; PRIOR APPLICATION NUMBER: 09/520,781

; PRIOR FILING DATE: 2000-03-03

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; PRIOR APPLICATION NUMBER: 60/123,667
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: 60/234,082
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: 60/233,798
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 60/174,485
; PRIOR FILING DATE: 2000-01-04
; PRIOR APPLICATION NUMBER: 10/403,676
; PRIOR FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: 60/371,002
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/384,798
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/402,407
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 60/443,062
; PRIOR FILING DATE: 2003-01-28
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 30
; LENGTH: 981
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-449-548-30

```

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Query Match          93.8%; Score 5113.5; DB 15; Length 981;
Best Local Similarity 94.6%; Pred. No. 0;
Matches 974; Conservative 0; Mismatches 1; Indels 55; Gaps 1;

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Qy      1 MRSEALLLYFTLLHFAGAGFPEDSEPISISHGNYTKQYPVFVGHKPGRNTTQRHRLDIQM 60
        |||
Db      4 MRSEALLLYFTLLHFAGAGFPEDSEPISISHGNYTKQYPVFVGHKPGRNTTQRHRLDIQM 63

Qy     61 IMIMNGTLYIAARDHIYTVDIDTSHTEEIYCSKKLTWKSQRQADVDTCRMKGKHKDECHNF 120
        |||
Db     64 IMIMNGTLYIAARDHIYTVDIDTSHTEEIYCSKKLTWKSQRQADVDTCRMKGKHKDECHNF 123

Qy    121 IKVLLKKND DALFVCGTNAFNPSCRNYKMDTLEPFGDEFSGMARCPYDAKHANVALFADG 180
        |||
Db    124 IKVLLKKND DALFVCGTNAFNPSCRNYKMDTLEPFGDEFSGMARCPYDAKHANVALFADG 183

Qy    181 KLYSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYFFFREIA 240
        |||
Db    184 KLYSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYFFFREIA 243

Qy    241 VEYNTMGKVVFPRVAQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDSHFYFNILQAVT 300
        |||
Db    244 VEYNTMGKVVFPRVAQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDSHFYFNILQAVT 303

Qy    301 DVIRINGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVPDER 360
        |||
Db    304 DVIRIKGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVPDER 363

Qy    361 VPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRL 420
        |||
Db    364 VPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRL 423

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Qy 421 TKIAVDTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLNDSL FLEEMSVYNSEKCSYD 480
 |||
 Db 424 TKIAVDTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLNDSL FLEEMSVYNSEKCSYD 483

Qy 481 GVEDKRIMGMLDRASSSLYVAFSTCVIKVPLGR CERH GKCKKTCIASRDPYCGWIKEGG 540
 |||
 Db 484 GVEDKRIMGMLDRASSSLYVAFSTCVIKVPLGR CERH GKCKKTCIASRDPYCGWIKEGG 543

Qy 541 ACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALNGHSSSLPSTTTSDSTAQEGYESR 600
 |||
 Db 544 ACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALN----- 579

Qy 601 GGMLDWKHL L DSPDST DPLGAVSSH NHQDKKGVIRESYLKGHDQLVPV TLLAIAVILAFV 660
 |||
 Db 580 -----GVIRESYLKGHDQLVPV TLLAIAVILAFV 608

Qy 661 MGA VFSGITVYCVCDHRRKDVAVVQRKEKELTHSRRGSMSSVTKL SGLFGDTQSKDPKPE 720
 |||
 Db 609 MGA VFSGITVYCVCDHRRKDVAVVQRKEKELTHSRRGSMSSVTKL SGLFGDTQSKDPKPE 668

Qy 721 AILTPLMHNGKLATPGNTAKMLIKADQHHLDTALPTPESTPTLQQKRKPSRGSREWERN 780
 |||
 Db 669 AILTPLMHNGKLATPGNTAKMLIKADQHHLDTALPTPESTPTLQQKRKPSRGSREWERN 728

Qy 781 QNLINACTKDMPPMGSPVIPTDLPLRASPSHIPSVVVLPI TQQGYQHEYVDQPKMSEVAQ 840
 |||
 Db 729 QNLINACTKDMPPMGSPVIPTDLPLRASPSHIPSVVVLPI TQQGYQHEYVDQPKMSEVAQ 788

Qy 841 MALEDQAATLEYKTIKEHLSSKSPNHGVNLVENLDSLPPKVPQREASLGPPGASLSQTGL 900
 |||
 Db 789 MALEDQAATLEYKTIKEHLSSKSPNHGVNLVENLDSLPPKVPQREASLGPPGASLSQTGL 848

Qy 901 SKRLEMHHSSSYGV DYKRSYPTNSLTRSHQATTLKRNTNSSNSSHL SRNQSFGRGDNPP 960
 |||
 Db 849 SKRLEMHHSSSYGV DYKRSYPTNSLTRSHQATTLKRNTNSSNSSHL SRNQSFGRGDNPP 908

Qy 961 PAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRTPSLKPDVPPKPSFAPLS 1020
 |||
 Db 909 PAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRTPSLKPDVPPKPSFAPLS 968

Qy 1021 TSMKPNDACT 1030
 |||
 Db 969 TSMKPNDACT 978

RESULT 15

US-10-403-676-46

; Sequence 46, Application US/10403676

; Publication No. US20040029150A1

; GENERAL INFORMATION:

; APPLICANT: Alsobrook II, John

; APPLICANT: Anderson, David W.

; APPLICANT: Boldog, Ferenc L.

; APPLICANT: Burgess, Catherine E.

; APPLICANT: Casman, Stacie J.

; APPLICANT: Edinger, Shlomit R.

; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Grosse, William M.
; APPLICANT: Guo, Xiaojia
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Ji, Weizhen
; APPLICANT: LaRochelle, William J.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Li, Li
; APPLICANT: Liu, Xiaohong
; APPLICANT: MacDougall, John R.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Millet, Isabelle
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Patturajan, Meera
; APPLICANT: Peyman, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Reiger, Daniel
; APPLICANT: Rothenberg, Mark E.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Stone, David J.
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Vernet, Corine
; APPLICANT: Zerhusen, Bryan D.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME,
AND METHODS OF USE
; FILE REFERENCE: 21402-573B
; CURRENT APPLICATION NUMBER: US/10/403,676
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: 60/123,667
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: 09/520,781
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 09/957,187
; PRIOR FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/371,002
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 09/538,092
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 09/604,286
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 60/140,584
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 60/370,381
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/384,297
; PRIOR FILING DATE: 2002-05-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 179
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 46
; LENGTH: 971
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-403-676-46

Query Match 93.8%; Score 5109.5; DB 12; Length 971;
Best Local Similarity 94.2%; Pred. No. 0;
Matches 970; Conservative 1; Mismatches 0; Indels 59; Gaps 1;

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Qy      1 MRSEALLLYFTLLHFAGAGFPEDSEPISISHGNYTKQYPVFVGHKPGRNTTQRHRLDIQM 60
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Db      1 MRSEALLLYFTLLHFAGAGFPEDSEPISISHGNYTKQYPVFVGHKPGRNTTQRHRLDIQM 60

Qy     61 IMIMNGTLYIAARDHIYTVDIDTSHTEEIYCSKKLTWKSQRQADVDCRMKGKHKDECHNF 120
      |||
Db     61 IMIMNGTLYIAARDHIYTVDIDTSHTEEIYCSKKLTWKSQRQADVDCRMKGKHKDECHNF 120

Qy    121 IKVLLKKND DALFVCGTNAFNPS CRNYKMDTLEPFGDEFSGMARCPYDAKHANVALFADG 180
      |||
Db    121 IKVLLKKND DALFVCGTNAFNPS CRNYKMDTLEPFGDEFSGMARCPYDAKHANVALFADG 180

Qy    181 KLYSATVTDFLAIDAVIYRSLGESPTLR TVKHDSKWLKEPYFVQAVDYGDIYFFFREIA 240
      |||
Db    181 KLYSATVTDFLAIDAVIYRSLGESPTLR TVKHDSKWLKEPYFVQAVDYGDIYFFFREIA 240

Qy    241 VEYNTMGKVVFPRVAQVCKNDMGGSQ RVLEKQWTSFLKARLNCSVPGDSHFYFNILQAVT 300
      |||
Db    241 VEYNTMGKVVFPRVAQVCKNDMGGSQ RVLEKRWTSFLKARLNCSVPGDSHFYFNILQAVT 300

Qy    301 DVIRINGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVPDER 360
      |||
Db    301 DVIRINGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVPDER 360

Qy    361 VPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRL 420
      |||
Db    361 VPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVR--- 417

Qy    421 TKIAVDTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLNDSL FLEEMSVYNSEKCSYD 480
      |||
Db    418 -----CSYD 421

Qy    481 GVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGR CERH GKCKKTCIASRDPYCGWIKEGG 540
      |||
Db    422 GVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGR CERH GKCKKTCIASRDPYCGWIKEGG 481

Qy    541 ACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALNGHSSSLLPSTTTSDSTAQEGYESR 600
      |||
Db    482 ACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALNGHSSSLLPSTTTSDSTAQEGYESR 541

Qy    601 GGMLDWKHLLDSPDSTDPLGAVSSH NHQDKKGVIRESYLKGHDQLVPV TLLAIAVILAFV 660
      |||
Db    542 GGMLDWKHLLDSPDSTDPLGAVSSH NHQDKKGVIRESYLKGHDQLVPV TLLAIAVILAFV 601

Qy    661 MGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRRGSMSSVTKLSGLFGDTQSKDPKPE 720
      |||
Db    602 MGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRRGSMSSVTKLSGLFGDTQSKDPKPE 661

Qy    721 AILTPLMHNGKLATPGNTAKMLIKADQHHL DLTALPTPESTPTLQQKRKPSRGSR EWERN 780
      |||
Db    662 AILTPLMHNGKLATPGNTAKMLIKADQHHL DLTALPTPESTPTLQQKRKPSRGSR EWERN 721

Qy    781 QNLINACTKDMPPMGSPVIPTDLPLRASPSHIPSVVVLPITQQGYQHEYVDQPKMSEVAQ 840
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Db	722	QNLINACTKDMPPMGSPVIPTDLPLRASPSHIPSVVVLPIITQQGYQHEYVDQPKMSEVAQ	781
Qy	841	MALEDQAATLEYKTIKEHLSSKSPNHGVNLVENLDSLPPKVPQREASLGPPGASLSQTGL	900
Db	782	MALEDQAATLEYKTIKEHLSSKSPNHGVNLVENLDSLPPKVPQREASLGPPGASLSQTGL	841
Qy	901	SKRLEMHHSSSYGVDYKRSYPTNSLTRSHQATTCLKRNNTNSSNSSHLNRNQSFGRGDNPP	960
Db	842	SKRLEMHHSSSYGVDYKRSYPTNSLTRSHQATTCLKRNNTNSSNSSHLNRNQSFGRGDNPP	901
Qy	961	PAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRTPSLKPDPVPPKPSFAPLS	1020
Db	902	PAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRTPSLKPDPVPPKPSFAPLS	961
Qy	1021	TSMKPNDACT	1030
Db	962	TSMKPNDACT	971

Search completed: March 24, 2004, 13:19:31
Job time : 77.7731 secs

Result		Query				Description
No.	Score	Match	Length	DB ID		

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2	3677	67.5	699	4	Q96SW4	Q96sw4 homo sapien
3	2980.5	54.7	574	4	Q96SM8	Q96sm8 homo sapien
4	2963	54.4	587	11	Q8BUT0	Q8but0 mus musculu
5	2961	54.3	605	11	Q8BXZ7	Q8bxz7 mus musculu
6	2952	54.2	562	4	Q96SY4	Q96sy4 homo sapien
7	2947	54.1	562	4	Q8NC49	Q8nc49 homo sapien
8	2621.5	48.1	507	4	Q96T04	Q96t04 homo sapien
9	2368	43.4	1073	4	Q8Nfy4	Q8nfy4 homo sapien
10	2349	43.1	1017	4	Q8Nfy5	Q8nfy5 homo sapien
11	2315.5	42.5	998	4	Q8Nfy6	Q8nfy6 homo sapien
12	2314	42.5	1011	4	Q8Nfy3	Q8nfy3 homo sapien
13	2314	42.5	1022	4	Q9P249	Q9p249 homo sapien
14	2309.5	42.4	1009	11	Q80TD0	Q80td0 mus musculu
15	2213	40.6	418	4	Q96JU9	Q96ju9 homo sapien
16	1908.5	35.0	595	11	Q8BKG8	Q8bkg8 mus musculu
17	1876.5	34.4	687	4	Q9BXR8	Q9bxr8 homo sapien
18	1611	29.6	476	4	Q8Nfy7	Q8nfy7 homo sapien
19	1526.5	28.0	963	11	Q91Y36	Q91y36 mus musculu
20	1480.5	27.2	452	13	Q7T165	Q7t165 brachydanio
21	1386.5	25.4	367	4	Q9HAH9	Q9hah9 homo sapien
22	1355.5	24.9	923	11	Q8R4U3	Q8r4u3 mus musculu
23	1320	24.2	920	11	Q8R4U4	Q8r4u4 rattus norv
24	1059	19.4	366	13	Q7ZV83	Q7zv83 brachydanio
25	856.5	15.7	770	5	O44253	O44253 drosophila
26	854.5	15.7	770	5	Q9V3M4	Q9v3m4 drosophila
27	847.5	15.6	774	13	Q8JIW9	Q8jiw9 xenopus lae
28	823.5	15.1	844	11	Q8BXU8	Q8bxu8 mus musculu
29	817.5	15.0	748	4	Q8TB71	Q8tb71 homo sapien
30	802.5	14.7	777	11	Q8BMF6	Q8bmf6 mus musculu
31	802.5	14.7	777	11	Q8BH34	Q8bh34 mus musculu
32	779.5	14.3	724	5	Q9V7Q7	Q9v7q7 drosophila
33	771	14.1	1122	11	Q7TT33	Q7tt33 mus musculu
34	768	14.1	697	5	Q8MLF1	Q8mlf1 drosophila
35	763	14.0	635	4	Q96GX0	Q96gx0 homo sapien
36	749	13.7	756	13	Q8QGU9	Q8qgu9 gallus gall
37	748	13.7	775	11	Q9QX23	Q9qx23 mus musculu
38	736.5	13.5	799	11	Q8BJC1	Q8bjc1 mus musculu
39	735.5	13.5	862	4	Q7Z5S4	Q7z5s4 homo sapien
40	694.5	12.7	616	5	Q9V7P8	Q9v7p8 drosophila
41	693	12.7	963	4	Q9C0C4	Q9c0c4 homo sapien
42	686	12.6	782	4	Q9NS98	Q9ns98 homo sapien
43	666.5	12.2	1083	5	Q9VTT0	Q9vtt0 drosophila
44	666.5	12.2	1091	5	Q7YU67	Q7yu67 drosophila
45	660	12.1	823	11	Q8BIR6	Q8bir6 mus musculu

ALIGNMENTS

RESULT 1

Q9EQ71

ID Q9EQ71 PRELIMINARY; PRT; 1005 AA.

AC Q9EQ71;

DT 01-MAR-2001 (TrEMBLrel. 16, Created)

DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Axon guidance signal SEMA6A1.
 GN SEMA6A.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=20564339; PubMed=10993894;
 RA Klostermann A., Lutz B., Gertler F., Behl C.;
 RT "The orthologous human and murine semaphorin 6A-1 proteins (SEMA6A-
 RT 1/Sema6A-1) bind to the Enabled/Vasodilator-stimulated Phosphoprotein-
 RT like Protein (EVL) via a novel carboxyl-terminal Zyxin-like domain.";
 RL J. Biol. Chem. 275:39647-39653(2000).
 DR EMBL; AF288666; AAG29494.1; -.
 DR MGD; MGI:1203727; Sema6a.
 DR GO; GO:0016021; C:integral to membrane; ISS.
 DR GO; GO:0008580; F:cytoskeletal regulator activity; ISS.
 DR GO; GO:0007411; P:axon guidance; ISS.
 DR GO; GO:0007166; P:cell surface receptor linked signal transdu. . .; ISS.
 DR GO; GO:0007399; P:neurogenesis; ISS.
 DR InterPro; IPR003659; Plexin-like.
 DR InterPro; IPR001627; Sema.
 DR Pfam; PF01403; Sema; 1.
 DR SMART; SM00423; PSI; 1.
 DR SMART; SM00630; Sema; 1.
 SQ SEQUENCE 1005 AA; 111758 MW; 57B69927F45B079D CRC64;

Query Match 92.2%; Score 5024.5; DB 11; Length 1005;
 Best Local Similarity 91.9%; Pred. No. 0;
 Matches 948; Conservative 26; Mismatches 30; Indels 27; Gaps 2;

Qy	1	MRSEALLLYFTLLHFAGAGFPEDSEPISISHGNYTKQYPVFGVGHKPGRNTTQRHRLDIQM	60
Db	1	MRPAALLLCLTLLHCAGAGFPEDSEPISISHGNYTKQYPVFGVGHKPGRNTTQRHRLDIQM	60
Qy	61	IMIMNGTLYIAARDHIYTVDIDTSHTEEIYCSKKLTWKSQRQADVDTCRMKGKHKDECHNF	120
		:	
Db	61	IMIMNRTLYVAARDHIYTVDIDTSHTEEIYCSKKLTWKSQRQADVDTCRMKGKHKDECHNF	120
Qy	121	IKVLLKKND DALFVCGTNAFNPSCRNYKMDTLEPGDEFSGMARCPYDAKHANVALFADG	180
		: :	
Db	121	IKVLLKKND DTLFVCGTNAFNPSCRNYRVDLTLETFGDEFSGMARCPYDAKHVNIALFADG	180
Qy	181	KLYSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYFFFREIA	240
		:	
Db	181	KLYSATVTDFLAIDAVIYRSPGDSPTLRTVKHDSKWLKEPYFVQAVDYGDIYFFFREIA	240
Qy	241	VEYNTMGKVVFPRVAQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDSHFYFNILQAVT	300
Db	241	VEYNTMGKVVFPRVAQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDSHFYFNILQAVT	300
Qy	301	DVIRINGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVPPER	360
Db	301	DVIRINGRDVVLATFSTPYNSIPGSAVCAYDMLDIADVFTGRFKEQKSPDSTWTPVPPER	360

Qy	361	VPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRL	420
		:	
Db	361	VPKPRPGCCAGSSSLEKYATSNEFPDDTLNFIKTHPLMDEAVPSIINRPWFLRTMVRYRL	420
Qy	421	TKIAVDTAAGPYQNHTVFLGSEKGIILKFLARIGNSGFLNDSLFLEEMSVYNSEKCSYD	480
		:	
Db	421	TKIAVDNAAGPYQNHTVV-----FLEEMNVYNPEKCSYD	454
Qy	481	GVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRCERHGKCKKTCIASRDPYCGWIKGG	540
		:	
Db	455	GVEDKRIMGMQLDRASGSLYVAFSTCVIKVPLGRCERHGKCKKTCIASRDPYCGWVRESG	514
Qy	541	ACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALNGHSSSLPSTTTSDSTAQEGYESR	600
		: : : : : : :	
Db	515	SCAHLSPLSRLTFEQDIERGNTDGLGDCHNSFVALNGHASSLYPNNTTSDSASRDGYESR	574
Qy	601	GGMLDWKHLSDSPDSTDPLGAVSSHNHQDKKGVIRESYLKGHDLVPTLLAIAVILAFV	660
		: : : : : :	
Db	575	GGMLDWNLDLEAPGSTDPLGAVSSHNHQDKKGVIRESYLKSNDQLVPTLLAIAVILAFV	634
Qy	661	MGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRRGSMSSVTKLSGLFGDTQSKDPKPE	720
		: : : : : :	
Db	635	MGAVFSGIIVYCVCDHRRKDVAVVRRKEKELTHSRRGSMSSVSELSGLFGDTQSKDPKPE	694
Qy	721	AILTPLMHNGKLATPGNTAKMLIKADQHHLDTALPTPESTPTLQQKRKPSRGSREWERN	780
		: : : : : :	
Db	695	AILTPLMHNGKLATSSNTAKMLIKADQHHLDTALPTPESTPTLQQKRKPNRGSREWERN	754
Qy	781	QNLINACTKDMPPMGSPVIPTDLPLRASPSHIPSVVVLPIITQQGYQHEYVDQPKMSE-VA	839
		:	
Db	755	QNIINACTKDMPPMGSPVIPTDLPLRASPSHIPSVVVLPIITQQGYQHEYVDQPKMSEVVA	814
Qy	840	QMALEDQAATLEYKTIKEHLSSKSPNHGVNLVENLDSLPPKVPQREASLGPPGASLSQTG	899
Db	815	QMALEDQAATLEYKTTKEHLSSKSPNHGVNLVENLDSLPPKVPQREASLGPPGTSLSQTG	874
Qy	900	LSKRLEMHSSSYGVYDKRSYPTNSLTRSHQATTLLKRNNNTNSSNSSHLNRNQSFGRGDNP	959
		: : : : : :	
Db	875	LSKRLEMQHSSSYGLEKYKRSYPTNSLTRSHQTTTLKRNNNTNSSNSSHLNRNQSFGRGDNP	934
Qy	960	PPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRTPSLKPDPVPPKPSFAPL	1019
Db	935	PPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRTPSLKPDPVPPKPSFAPL	994
Qy	1020	STSMKPNDACT	1030
Db	995	STSMKPNDACT	1005

RESULT 2

Q96SW4

ID Q96SW4 PRELIMINARY; PRT; 699 AA.

AC Q96SW4;

DT 01-DEC-2001 (TrEMBLrel. 19, Created)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE Hypothetical protein FLJ14595.

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
 RA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
 RA Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
 RA Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
 RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
 RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
 RA Ninomiya K., Iwayanagi T.;
 RT "NEDO human cDNA sequencing project.";
 RL Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AK027501; BAB55158.1; -.
 DR GO; GO:0007275; P:development; IEA.
 DR InterPro; IPR003659; Plexin-like.
 DR InterPro; IPR001627; Sema.
 DR Pfam; PF01403; Sema; 1.
 DR SMART; SM00423; PSI; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 699 AA; 76723 MW; 2E5F111D59741394 CRC64;

Query Match 67.5%; Score 3677; DB 4; Length 699;
 Best Local Similarity 100.0%; Pred. No. 4.5e-291;
 Matches 699; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	332	MLDIASVFTGRFKEQKSPDSTWTPVPDERVPKPRPGCCAGSSSLERYATSNEFPDDTLNF	391
Db	1	MLDIASVFTGRFKEQKSPDSTWTPVPDERVPKPRPGCCAGSSSLERYATSNEFPDDTLNF	60
Qy	392	IKTHPLMDEAVPSIFNRPWFLRTMVRYRLTKIAVDTAAGPYQNHTVVFLGSEKGIILKFL	451
Db	61	IKTHPLMDEAVPSIFNRPWFLRTMVRYRLTKIAVDTAAGPYQNHTVVFLGSEKGIILKFL	120
Qy	452	ARIGNSGFLNDSLFLEEMSVYNSEKCSYDGVEDKRIMGMQLDRASSSLYVAFSTCVIKVP	511
Db	121	ARIGNSGFLNDSLFLEEMSVYNSEKCSYDGVEDKRIMGMQLDRASSSLYVAFSTCVIKVP	180
Qy	512	LGR CERH GKCKKTCIASRDPYCGWIKEGGACSHLSPNSRLTFEQDIERGNTDGLGDCHNS	571
Db	181	LGR CERH GKCKKTCIASRDPYCGWIKEGGACSHLSPNSRLTFEQDIERGNTDGLGDCHNS	240
Qy	572	FVALNGHSSSLPSTTTSDSTAQEGYESRGGMLDWKHLLDSPDSTDPLGAVSSHNDKDK	631
Db	241	FVALNGHSSSLPSTTTSDSTAQEGYESRGGMLDWKHLLDSPDSTDPLGAVSSHNDKDK	300
Qy	632	GVIRESYLKGH DQLVPVTL LAIAVILAFVMGAVFSGITVYCVCDHRRKDVA VQRKEKEL	691
Db	301	GVIRESYLKGH DQLVPVTL LAIAVILAFVMGAVFSGITVYCVCDHRRKDVA VQRKEKEL	360
Qy	692	THSR RGSMS SVTKLSGLFGDTQSKDPKPEAILT PLMHNGKLATPGNTAKMLIKADQHHL D	751
Db	361	THSR RGSMS SVTKLSGLFGDTQSKDPKPEAILT PLMHNGKLATPGNTAKMLIKADQHHL D	420
Qy	752	LTALPTPESTPTLQQKRKPSRGSREWERNQNLINACTKDMPPMGSPVIPTDLPLRASPSH	811

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Db      421  |LTALPTPESTPTLQQKQKPSRGSREWERNQNLINACTKDMPPMGSPVIPTDLPLRASPSH| 480
Qy      812  |IPSVVVLPIITQQGYQHEYVDQPKMSEVAQMALEDQAATLEYKTIKEHLSSKSPNHGVNLV| 871
Db      481  |IPSVVVLPIITQQGYQHEYVDQPKMSEVAQMALEDQAATLEYKTIKEHLSSKSPNHGVNLV| 540
Qy      872  |ENLDSLPPKVPQREASLGPPGASLSQTGLSKRLEMHHSSSYGVDYKRSYPTNSLTRSHQA| 931
Db      541  |ENLDSLPPKVPQREASLGPPGASLSQTGLSKRLEMHHSSSYGVDYKRSYPTNSLTRSHQA| 600
Qy      932  |TTLKRNTNTSSNSSHLNRNQSFGRGDNPPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNA| 991
Db      601  |TTLKRNTNTSSNSSHLNRNQSFGRGDNPPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNA| 660
Qy      992  |YNSLTRSGLKRTPSLKPDPVPPKPSFAPLSTSMKPNDACT| 1030
Db      661  |YNSLTRSGLKRTPSLKPDPVPPKPSFAPLSTSMKPNDACT| 699

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RESULT 3

Q96SM8

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ID  Q96SM8      PRELIMINARY;      PRT;      574 AA.
AC  Q96SM8;
DT  01-DEC-2001 (TrEMBLrel. 19, Created)
DT  01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT  01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE  Hypothetical protein FLJ14748.
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX  NCBI_TaxID=9606;
RN  [1]
RP  SEQUENCE FROM N.A.
RA  Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA  Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
RA  Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA  Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
RA  Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
RA  Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
RA  Ninomiya K., Iwayanagi T.;
RT  "NEDO human cDNA sequencing project.";
RL  Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
DR  EMBL; AK027654; BAB55269.1; -.
DR  GO; GO:0007275; P:development; IEA.
DR  InterPro; IPR003659; Plexin-like.
DR  SMART; SM00423; PSI; 1.
KW  Hypothetical protein.
SQ  SEQUENCE 574 AA; 62822 MW; 0C79E01A4117A495 CRC64;

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Query Match      54.7%;  Score 2980.5;  DB 4;  Length 574;
Best Local Similarity  90.7%;  Pred. No. 2.5e-234;
Matches 574;  Conservative 0;  Mismatches 0;  Indels 59;  Gaps 1;

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Qy      398  |MDEAVPSIFNRPWFLRTMVRYLTKIAVDTAAGPYQNHTVVFLGSEKGIILKFLARIGNS| 457
Db      1    |MDEAVPSIFNRPWFLRTMVR-----| 20

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Qy	458	GFLNDSLFLLEMSVYNSEKCSYDGVEDKRIMGMLDRASSSLYVAFSTCVIKVPLGRCER	517
Db	21	-----CSYDGVEDKRIMGMLDRASSSLYVAFSTCVIKVPLGRCER	61
Qy	518	HGKCKKTCIASRDPYCGWKEGGACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALNG	577
Db	62	HGKCKKTCIASRDPYCGWKEGGACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALNG	121
Qy	578	HSSSLLPSTTTSDSTAQEGYESRGGMLDWKHLSDPDSTDPLGAVSSHNHQDKKGVIRE	637
Db	122	HSSSLLPSTTTSDSTAQEGYESRGGMLDWKHLSDPDSTDPLGAVSSHNHQDKKGVIRE	181
Qy	638	YLKGHDLQVLPVTLIAIVILAFVMGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRRG	697
Db	182	YLKGHDLQVLPVTLIAIVILAFVMGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRRG	241
Qy	698	SMSSVTKLSGLFGDTQSKDPKPEAILTPLMHNGKLATPGNTAKMLIKADQHHLDTALPT	757
Db	242	SMSSVTKLSGLFGDTQSKDPKPEAILTPLMHNGKLATPGNTAKMLIKADQHHLDTALPT	301
Qy	758	PESTPTLQQKRKPSRGSREWERNQNLINACTKDMPPMGSPVIPTDLPLRASPSHIPSVVV	817
Db	302	PESTPTLQQKRKPSRGSREWERNQNLINACTKDMPPMGSPVIPTDLPLRASPSHIPSVVV	361
Qy	818	LPITQQGYQHEYVDQPKMSEVAQMALEDQAATLEYKTIKEHLSSKSPNHGVNLVENLDSL	877
Db	362	LPITQQGYQHEYVDQPKMSEVAQMALEDQAATLEYKTIKEHLSSKSPNHGVNLVENLDSL	421
Qy	878	PPKVPQREASLGPPGASLSQTGLSKRLEMHHSSSYGVYKRSYPTNSLTRSHQATTLKRN	937
Db	422	PPKVPQREASLGPPGASLSQTGLSKRLEMHHSSSYGVYKRSYPTNSLTRSHQATTLKRN	481
Qy	938	NTNSSNSSHLNRNQSFGRGDNPPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTR	997
Db	482	NTNSSNSSHLNRNQSFGRGDNPPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTR	541
Qy	998	SGLKRTPSLKPDPVPPKPSFAPLSTSMKPNDACT	1030
Db	542	SGLKRTPSLKPDPVPPKPSFAPLSTSMKPNDACT	574

RESULT 4

Q8BUT0

ID Q8BUT0 PRELIMINARY; PRT; 587 AA.
AC Q8BUT0;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Sema domain.
GN A730020P05RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK082711; BAC38582.1; -.
DR MGD; MGI:2443196; A730020P05Rik.
DR InterPro; IPR001627; Sema.
DR Pfam; PF01403; Sema; 1.
DR SMART; SM00630; Sema; 1.
SQ SEQUENCE 587 AA; 66044 MW; EB9C7B102C4DB97A CRC64;

Query Match 54.4%; Score 2963; DB 11; Length 587;
Best Local Similarity 95.1%; Pred. No. 7e-233;
Matches 549; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

Qy	1	MRSEALLLYFTLLHFAGAGFPEDSEPISISHGNYTKQYPVFGHKPGRNTTQRHRLDIQM	60
Db	1	MRPAALLLCLTLLHCAGAGFPEDSEPISISHGNYTKQYPVFGHKPGRNTTQRHRLDIQM	60
Qy	61	IMIMNGTLYIAARDHIYTVDIDTSHTEEIYCSKKLTWKSQRQADVDCRMKGKHKDECHNF	120
		:	
Db	61	IMIMNRTLYVAARDHIYTVDIDTSHTEEIYCSKKLTWKSQRQADVDCRMKGKHKDECHNF	120
Qy	121	IKVLLKKND DALFVCGTNAFNPS CRNYKMDTLEPFGDEFSGMARCPYDAKHANVALFADG	180
		: :	
Db	121	IKVLLKKND DTLFVCGTNAFNPS CRNYRVDTLETFGDEFSGMARCPYDAKHANIALFADG	180
Qy	181	KLYSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYFFFREIA	240
		:	
Db	181	KLYSATVTDFLAIDAVIYRSLGDSPTLRTVKHDSKWLKEPYFVQAVDYGDIYFFFREIA	240
Qy	241	VEYNTMGKVVFP RVAQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDSHFYFNILQAVT	300
Db	241	VEYNTMGKVVFP RVAQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDSHFYFNILQAVT	300
Qy	301	DVIRINGR DVVLATFSTPYNSIPGS AVCAYDMLDIASVFTGRFKEQKSPDSTWTPVPDER	360
		:	
Db	301	DVIRINGR DVVLATFSTPYNSIPGS AVCAYDMLDIANVFTGRFKEQKSPDSTWTPVPDER	360
Qy	361	VPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRL	420
		: :	
Db	361	VPKPRPGCCAGSSSLEKYATSNEFPDDTLNFIKTHPLMDEAVPSIINRPWFLRTMVRYRL	420
Qy	421	TKIAVDTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLNDSLFL EEMSVYNSEKCSYD	480
		: :	
Db	421	TKIAVDNAAGPYQNHTVVFLGSEKGIILKFLARIGSSGFLNGSLFL EEMNVYNPEKCSYD	480
Qy	481	GVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGR CERH GKCKKTCIASRDPYCGWIKEGG	540
		:	
Db	481	GVEDKRIMGMQLDRASGSLYVAFSTCVIKVPLGR CERH GKCKKTCIASRDPYCGWVRESG	540
Qy	541	ACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALNG	577
		: :	
Db	541	SCAHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALNG	577

RESULT 5

Q8BXZ7

ID Q8BXZ7 PRELIMINARY; PRT; 605 AA.
 AC Q8BXZ7;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Sema domain.
 GN A730020P05RIK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
 RX MEDLINE=22354683; PubMed=12466851;
 RA The FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 DR EMBL; AK042751; BAC31351.1; -.
 DR MGD; MGI:2443196; A730020P05Rik.
 DR InterPro; IPR001627; Sema.
 DR Pfam; PF01403; Sema; 1.
 DR SMART; SM00630; Sema; 1.
 SQ SEQUENCE 605 AA; 68299 MW; B4FE713BE8AF6E90 CRC64;

Query Match 54.3%; Score 2961; DB 11; Length 605;
 Best Local Similarity 94.5%; Pred. No. 1.1e-232;
 Matches 550; Conservative 14; Mismatches 18; Indels 0; Gaps 0;

Qy 1 MRSEALLLYFTLLHFAGAGFPEDSEPISSISHGNYTKQYPVFVGHKPGRNTTQRHRLDIQM 60
 || |||| |||| ||||||||||||||||||||||||||||||||||||||||
 Db 1 MRPAALLLCLTLLHCAGAGFPEDSEPISSISHGNYTKQYPVFVGHKPGRNTTQRHRLDIQM 60

Qy 61 IMIMNGTLYIAARDHIYTVDIDTSHTEEIYCSKKLTWKSQRQADVDTCRMKGKHKDECHNF 120
 ||||| |||:||||||||||||||||||||||||||||||||||||||
 Db 61 IMIMNRTLYVAARDHIYTVDIDTSHTEEIYCSKKLTWKSQRQADVDTCRMKGKHKDECHNF 120

Qy 121 IKVLLKKND DALFVCGTNAFNPSCRNYKMDTLEPFGDEFSGMARCPYDAKHANVALFADG 180
 ||||| ||||| ||||||||||||||||:|||| |||||||||||||||||||:|||||
 Db 121 IKVLLKKNDT LFVCGTNAFNPSCRNYRVDLTLETFGDEFSGMARCPYDAKHANIALFADG 180

Qy 181 KLYSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLEKPYFVQAVDYGDIYFFFREIA 240
 ||||||||||||||||||||:||||||||||||||||||||||||||||||
 Db 181 KLYSATVTDFLAIDAVIYRSLGDSPTLRTVKHDSKWLEKPYFVQAVDYGDIYFFFREIA 240

Qy 241 VEYNTMGKVVFP RVAQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDSHFYFNILQAVT 300
 ||||||||||||||||||||||||||||||||||||||||||||||||
 Db 241 VEYNTMGKVVFP RVAQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDSHFYFNILQAVT 300

Qy 301 DVIRINGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVPDER 360
 ||||||||||||||||||||||||||||||||:||||||||||||||||||

Db	301	DVIRINGRDVVLATFSTPYNSIPGSAVCAYDMLDIANVFTGRFKEQKSPDSTWTPVPDER	360
Qy	361	VPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRL	420
		:	
Db	361	VPKPRPGCCAGSSSLEKYATSNEFPDDTLNFIKTHPLMDEAVPSIINRPWFLRTMVRYRL	420
Qy	421	TKIAVDTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLNDSLFLLEMSVYNSEKCSYD	480
		: :	
Db	421	TKIAVDNAAGPYQNHTVVFLGSEKGIILKFLARIGSSGFLNGSLFLEEMNVYNPEKCSYD	480
Qy	481	GVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRCERHGKCKKTCIASRDPYCGWIKEGG	540
		:	
Db	481	GVEDKRIMGMQLDRASGSLYVAFSTCVIKVPLGRCERHGKCKKTCIASRDPYCGWVRESG	540
Qy	541	ACSHLSPNSRLTTFEQDIERGNTDGLGDCHNSFVALNGHSSSL	582
		: : :	
Db	541	SCAHLSPLSRLTTFEODIERGNTDGLGDCHNSFVALNDISTPL	582

Q96SY4

AC Q96SY4;

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DE Hypothetical protein FLJ14565.

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

RN [1]

RA Isoqai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,

RA Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,

BA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,

RA Ninomiya K., Iwayanagi T.;

RT "NEDO human cDNA sequencing project.";

DR EMBL; AK027471; BAB55136.1; -.

DR GO; GO:0007275; P:development; IEA.

DR InterPro; IPR003659; Plexin-like.

DR SMART; SM00423; PSI; 1.

SO SEQUENCE 562 AA; 61313 MW; 6AB3685FAD1DD78A CRC64;

Qy 469 MSVYNSEKCSYDGVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRCERHGKCKKTCIAS 528

Db 1 MSVYNSEKCSYDGVEDKRIMGMOLDRASSSLYVAFSTCVIKVPLGR CERH GKCKKTCIAS 60

Qy	529	RDPCGWIKEGGACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALNGHSSSLLPSTTT	588
Db	61	RDPCGWIKEGGACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALNGHSSSLLPSTTT	120
Qy	589	SDSTAQEGYESRGGMLDWKHLSDPDSTDPLGAVSSHNHQDKKGVIRESYLKGHDLVPV	648
Db	121	SDSTAQEGYESRGGMLDWKHLSDPDSTDPLGAVSSHNHQDKKGVIRESYLKGHDLVPV	180
Qy	649	TLLAIAVILAFVMGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRGSMSSVTKLSGL	708
Db	181	TLLAIAVILAFVMGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRGSMSSVTKLSGL	240
Qy	709	FGDTQSKDPKPEAILTPLMHNGKLATPGNTAKMLIKADQHHLDTALPTPESTPTLQQR	768
Db	241	FGDTQSKDPKPEAILTPLMHNGKLATPGNTAKMLIKADQHHLDTALPTPESTPTLQQR	300
Qy	769	KPSRGSREWERNQNLINACTKDMPPMGSPVIPTDLPLRASPSHIPSVVVLPIITQQGYQHE	828
Db	301	KPSRGSREWERNQNLINACTKDMPPMGSPVIPTDLPLRASPSHIPSVVVLPIITQQGYQHE	360
Qy	829	YVDQPKMSEVAQMALEDQAATLEYKTIKEHLSSKSPNHGVNLVENLDSLPPKVPQREASL	888
Db	361	YVDQPKMSEVAQMALEDQAATLEYKTIKEHLSSKSPNHGVNLVENLDSLPPKVPQREASL	420
Qy	889	GPPGASLSQTGLSKRLEMHHSSSYGVYDKRSYPTNSLTRSHQATTCLKRNNTNSSNSSHLS	948
Db	421	GPPGASLSQTGLSKRLEMHHSSSYGVYDKRSYPTNSLTRSHQATTCLKRNNTNSSNSSHLS	480
Qy	949	RNQSFGRGDNPPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRTPSLKP	1008
Db	481	RNQSFGRGDNPPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRTPSLKP	540
Qy	1009	DVPPKPSFAPLSTSMKPNDACT	1030
Db	541	DVPPKPSFAPLSTSMKPNDACT	562

RESULT 7

Q8NC49

ID Q8NC49 PRELIMINARY; PRT; 562 AA.

AC Q8NC49;

DT 01-OCT-2002 (TrEMBLrel. 22, Created)

DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)

DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)

DE Hypothetical protein FLJ90494.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RA Isogai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T.,

RA Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K.,

RA Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahari K.,

RA Masuho Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N.,

RA Hattori A., Okumura K., Iwayanagi T., Ninomiya K.;

RT "NEDO human cDNA sequencing project.";

RL Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AK074975; BAC11326.1; -.
KW Hypothetical protein.
SQ SEQUENCE 562 AA; 61286 MW; 708041459E34D78A CRC64;

Query Match 54.1%; Score 2947; DB 4; Length 562;
Best Local Similarity 99.8%; Pred. No. 1.3e-231;
Matches 561; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy      469 MSVYNSEKCSYDGVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRGERHGKCKKTCIAS 528
          |||
Db      1 MSVYNSEKCSYDGVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRGERHGKCKKTCIAS 60

Qy      529 RDPYCGWIKEGGACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALNGHSSSLPSTTT 588
          |||
Db      61 RDPYCGWIKEGGACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALNGHSSSLPSTTT 120

Qy      589 SDSTAQEGYESRGGMLDWKHLSDSPDSTDPLGAVSSHNHQDKKGVIRESYLKGHDLVPV 648
          |||
Db      121 SDSTAQEGYESRGGMLDWKHLSDSPDSTDPLGAVSSHNHQDKKGVIRESYLKGHDLVPV 180

Qy      649 TLLAIAVILAFVMGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRGSMSSVTKLSGL 708
          |||
Db      181 TLLAIAVILAFVMGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRGSMSSVTKLSGL 240

Qy      709 FGDTQSKDPKPEAILTPLMHNGKLATPGNTAKMLIKADQHHLDTALPTPESTPTLQQR 768
          |||
Db      241 FGDTQSKDPKPEAILTPLMHNGKLATPGNTAKMLIKADQHHLDTALPTPESTPTLQQR 300

Qy      769 KPSRGSREWERNQNLINACTKDMPPMGSPVIPTDLPLRASPSHIPSVVVLPIITQQGYQHE 828
          |||
Db      301 KPSRGSREWERNQNLINACTKDMPPMGSPVIPTDLPLRASPSHIPSVVVLPIITQQGYQHE 360

Qy      829 YVDQPKMSEVAQMALEDQAATLEYKTIKEHLSSKSPNHGVNLVENLDSLPPKVPQREASL 888
          |||
Db      361 YVDQPKMSEVAQMALEDQAATLEYKTIKEHLSSKSPNHGVNLVENLDSLPPKVPQREASL 420

Qy      889 GPPGASLSQTGLSKRLEMHHSSSYGVYDKRSYPTNSLTRSHQATTLKRNTNSSNSSHLS 948
          |||
Db      421 GPPGASLSQTGLSKRLEMHHSSSYGVYDKRSYPTNSLTRSHQATTLKRNTNSSNSSHLS 480

Qy      949 RNQSFGRGDNPPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRTPSLKP 1008
          |||
Db      481 RNQSFGRGDSPPPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRTPSLKP 540

Qy      1009 DVPPKPSFAPLSTSMKPNDACT 1030
          |||
Db      541 DVPPKPSFAPLSTSMKPNDACT 562
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RESULT 8

Q96T04

ID Q96T04 PRELIMINARY; PRT; 507 AA.

AC Q96T04;

DT 01-DEC-2001 (TrEMBLrel. 19, Created)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

Db 366 GPPGASLSQTGLSKRLEMHHSSSYGVYKRSYPTNSLTRSHQATTCLKRNNTNSSNSSHLS 425

Qy 949 RNQSFGRGDNPPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRTPSLKP 1008
 |||||

Db 426 RNQSFGRGDNPPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRTPSLKP 485

Qy 1009 DVPPKPSFAPLSTSMKPNDACT 1030
 |||||

Db 486 DVPPKPSFAPLSTSMKPNDACT 507

RESULT 9

Q8NFY4

ID Q8NFY4 PRELIMINARY; PRT; 1073 AA.
 AC Q8NFY4;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Semaphorin 6D isoform 4.
 GN SEMA6D.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Qu X., Zhai Y., Wei H., Yu Y., Tang F., He F.;
 RT "Homo sapiens semaphorin 6D isoform 4 (SEMA6D.4) mRNA, complete cds.";
 RL Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF389429; AAM69452.1; -.
 DR InterPro; IPR001627; Sema.
 DR Pfam; PF01403; Sema; 1.
 DR SMART; SM00630; Sema; 1.
 SQ SEQUENCE 1073 AA; 119872 MW; 7DCE4DFC5BF70F9E CRC64;

Query Match 43.4%; Score 2368; DB 4; Length 1073;
 Best Local Similarity 46.0%; Pred. No. 7.5e-184;
 Matches 512; Conservative 159; Mismatches 308; Indels 134; Gaps 30;

Qy 1 MRSEALLLYFTLL---HFAGAGFPEDSEPISISHGNYTKQYPVFVGHKPGRNTTQRHRLD 57
 || | | || |||| ||:: :||:|||| | :| | :| ||||

Db 1 MRVFLLCAYILLMLVSQLRAVSFPEDDEPLNTVDYHYSRQYPVFRG-RPSGNESQ-HRLD 58

Qy 58 IQMIMIMNGTLYIAARDHIYTVDIDTSHTEEIYCSKKLTWKSQRQADVDTCRMKGKHKDEC 117
 |::: : |||| | | :||::: | : :|||:| | : | |||||

Db 59 FQLMLKIRDITLYIAGRDQVYTVNLNEMPKEVIPNKKLTWRSRQQDRENCAMKGKHKDEC 118

Qy 118 HNFIVKLLKKNDALFVCGTNAFNPSCRNYKMDTLEPFGDEFSGMARCPYDAKHANVALF 177
 ||||| : :||: :||| |||| | | |:: || | :| ||:||||:|: | ||||

Db 119 HNFIVKVFVRNDEMVFVCGTNAFNPSCRNYRLSTLEYDGEEISGLARCPFDARQTNVALF 178

Qy 178 ADGKLYSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYFFFR 237
 ||||| |||| |||||:|: |||:|:|:|:|:|: |::|:|:|:|:|

Db 179 ADGKLYSATVADFLASDAVIYRSMGDGSALRTIKYDSKWIKEPHFLHAIEYGNVYFFFR 238

Qy 238 EIAVEYNTMGKVVFPRVAQVCKNDMGGSQRVLEKQWTSFLKARLNCVPGDSHFYFNILQ 297

Db	239	EIAVEHNNLGKAVYSRVARICKNDMGGSQRVLEKHWTSFLKARLNCSVPGDSFFYFDVLQ	298
Qy	298	AVTDVIRINGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVP	357
Db	299	SITDIIQINGIPTVVGVFTTQLNSIPGSAVCAFSMDIEKVFKEQKTPDSVWTAVP	358
Qy	358	DERVPKPRPGCCAGSSSLERYATSNEFPDDLNFIKTHPLMDEAVPSIFNRPWFLRTMVR	417
Db	359	EDKVPKPRPGCCAKHGLAEAYKTSIDFPDETLFSIKSHPLMDSAVPPIADEPWFTKTRVR	418
Qy	418	YRLTKIAVDTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGF-LNDSLFLLEEMSVYNSEK	476
Db	419	YRLTAISVDHSAGPYQNYTVIFVGSEAGMVLKVLAK--TSPFSLNDSVLLEEIEAYNHAK	476
Qy	477	CSYDGVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRCERHGKCKKTCIASRDPYCGWI	536
Db	477	CSAENEDKKVISLQLDKDHHALYVAFSSCIIRIPLSRCERYGSKCKSCIASRDPYCGWL	536
Qy	537	KEGGACSHLSPNSRLT-FEQDIERGNTDGLGDCHNSFVALNGHSSSLPSTTTSDSTAQE	595
Db	537	SQ-GSCGRVTPGMLAEGYEQDTEFGNTAHLGDCH-----EILPTSTTPD-----	579
Qy	596	GYESRGG-----MLD-WKHLL-----DSP---DSTD	618
Db	580	-YKIFGGPTSDMEVSSSVTTMASIPEITPKVIDTWRPKLTSSRKFFVQDDPNTSDFTDP	638
Qy	619	LGAVSSHNHQDKKGVIRESYLKGDHQLVPTLLAIAVILAFVMGAVFSGITVYCVCD-HR	677
Db	639	LSGI-----PKGVRWEVQSGESNQMVHMNVLITCVFAAFVLGAFIAGVAVYCYRDMFV	691
Qy	678	RKDVAVVQRKEKELTHSRGSMSSVTKLSGLFG---DTQSKDPKPEAILTPLMHNGKLA	733
Db	692	RKNRKI--HKDAESAQSCTDSSGSFAKLNGLFDSVPVKEYQQNIDSPKLYSNLLTSRKELP	749
Qy	734	TPGNTAKMLIKADQHHLDTALPTPESTPTLQQKRKPSRGSREWERNQNINACTKDMPP	793
Db	750	PNGDTKSMVMDHRGQPPELAALPTPESTPVLHQKTLQAMKSHSEKAHGH--GASRKETPQ	807
Qy	794	MGSPVIPTDLPLRASPSHIPSVVVLPTQQGYQHEY-----VDQP---KMS	836
Db	808	FFPSSPPPHSPL--SHGHIPSAIVLPNATHDYNTSFSNSNAHKAEEKLQNDHPLTKSSS	865
Qy	837	EVAQMALEDQAATLEYKTIKEHLSSKSPN-----HGVNLVENLDSL---PPKVP	882
Db	866	KRDHRRSVDSRNTL--NDLLKHLNDPNSNPKAIMGDIQMAHQNLMLDPMGMSSEVPKVP	923
Qy	883	QREASLGPPGASLSQTGLSKRLEMHHSSSY---GVDYKRSYPTNSLTRSHQATTIKRNT	939
Db	924	NREASLYSPSTLPRNSPTKRVDVPTPGVPMTSLERQRGYHKNSSQR-HSISAMPK-NL	981
Qy	940	NSSNSSHLSRNQSFGRGD-NPPAPQVRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLT--	996
Db	982	NSPNGVLLSRQPSMNRGGYMPPTGAKVDYIQ-----GTPVSVHLQPSLSRQSSYTSN	1034
Qy	997	----RSGLKRTPSLKPDPVPPKPSFAPLSTSMKP	1025


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      :::||||||| | | | :||:|:|:|:| | | | : | | : | |
Db      359 EDKVPKPRPGCCAKHGLAEAYKTSIDFPDETLSEFIKSHPLMDSAVPPIADEPWFTKTRVR 418
Qy      418 YRLTKIAVDTAAGPYQNHTVVLGSEKGIILKFLARIGNSGF-LNDSLFLLEEMSVYNSEK 476
      ||| | :| | :| | | | :| | :| | | :| | | | : | | |
Db      419 YRLTAISVDHSAGPYQNYTVIFVGSEAGMVLKVLAK--TSPFSLNDSVLLLEEIEAYNHAK 476
Qy      477 CSYDGVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRRCERHGKCKKTCIASRDPYCGWI 536
      || : | | : : : | | : | | | | :| | : | | | | | | :
Db      477 CSAENEEDKKVISLQLDKDHHALYVAFSSCIIRIPLSRCERYGSCKKSCIASRDPYCGWL 536
Qy      537 KEGGACSHLSPNSRLT-FEQDIERGNTDGLGDCHNSFVALNGHSSSLPSTTTSDSTAQE 595
      : | : | : | : | | | | | | | | | | : | | : | | |
Db      537 SQ-GSCGRVTPGMLAEGYEQDTEFGNTAHLGDCH-----EILPTSTTPD----- 579
Qy      596 GYESRGGMLDWKHLSDSPDSTDPLGAVSSHNDKKGVIRESYLKQHDQLVPVTLIAIAV 655
      | : | | | | | | | | | | | | | | | | | | : | : | |
Db      580 -YKIFGG-----PTS-----GVRWEVQSGESNQMVHNMVNLITCV 612
Qy      656 ILAFVMGAVFSGITVYCVCD-HRRKDVAVVQRKEKELTHSRRGSMSSVTKLSGLFG---- 710
      ||| : | : | | | | | : | : | | | | | | | | | |
Db      613 FAAFVLGAFIAGVAVYCYRDMFVRKNRKI--HKDAESAQSCTDSSGSFAKLNGLFDSPVK 670
Qy      711 DTQSKDPKPEAILTPLMHNGKLATPGNTAKMLIKADQHHLDLTALPTPESTPTLQQKRKP 770
      : | : | | : | | : | | : | | | | | | | | | |
Db      671 EYQQNIDSPKLYSNLLTSRKELPPNGDTKSMVMDHRGQPPELAALPTPESTPVLHQKTLQ 730
Qy      771 SRGSREWERNQNINACTKDMPPMGSPVIPTDLPLRASPSHIPSVVVLPIITQQGYQHEY- 829
      : | : : : | : | | | | | | | | | | | | | | :
Db      731 AMKSHSEKAHGH--GASRKETPQFFPSSPPPHSPL--SHGHIPSAIVLPNATHDYNTSFS 786
Qy      830 -----VDQP---KMSEVAQMALEDQAATLEYKTIKEHLSSKSPN----- 865
      : | | | : | | | | : | | : | | : |
Db      787 NSNAHKAEEKLQNIDHPLTKSSSKRDHRRSVDSRNTL--NDLLKHLNDPNSNPKAIMGDI 844
Qy      866 ---HGVNLVENLDSL---PPKVPQREASLGPPGASLSQTGLSKRLEMHHSSSY---GVDY 916
      | : : : | : | | | | | | | | | | | | | | : :
Db      845 QMAHQNLMLDPMGSMSEVPKVENREASLYSPSTLPRNSPTKRVDVPTTPGVPMTSLER 904
Qy      917 KRSYPTNSLTRSHQATTLKRNNNTSSNSSHLNRNQSFGRGD-NPPAPQVRVDSIQVHSSQ 975
      : | | | | : : : | | | | | | | | | | : | | |
Db      905 QRGYHKNSSQR-HSISAMPK-NLNSPENGVLNLSRQPSMNRGGYMPPTPTGAKVDYIQ----- 957
Qy      976 PSGQAVTVSRQPSLNAYNSLT-----RSGLKRTPSLKPDPVPPKPSFAPLSTSMKP 1025
      | | : | | | : | | | : | | | | | | | | | | | : | : |
Db      958 --GTPVSVHLQPSLSRQSSYTSNGTLPRGTGLKRTPSLKPDPVPPKPSFVPQTPSVRP 1011

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RESULT 11

Q8NFY6

ID Q8NFY6 PRELIMINARY; PRT; 998 AA.

AC Q8NFY6;

DT 01-OCT-2002 (TrEMBLrel. 22, Created)

DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

DE Semaphorin 6D isoform 2.

GN SEMA6D.


```

      : |:| ::| :||| | ||| |||||
Db      537 SQ-GSCGRVTPGMLAEGYEQDTEFGNTAHLGDCHG----- 570

Qy      596 GYESRGGMLDWKHLSDSPDSTDPLGAVSSSHNHQDKKGVIRESYLKGHDLVPVTLTLLAIAV 655
      : |:| :| :| :||| : :| |
Db      571 -----VRWE--VQSGES-----NQMVHNMVLTITCV 593

Qy      656 ILAFVMGAVFSGITVYCVCD-HRRKDVAVVQRKEKELTHSRGSMSSVTKLSGLFG---- 710
      |||:| :|: ||| | ||: : |:| | | | ||:|
Db      594 FAAFVLGAFIAGVAVYCYRDMFVRKNRKI--HKDAESAQSCTDSSGSFAKLNGLFDSPVK 651

Qy      711 DTQSKDPKPEAILTPLMHNGKLATPGNTAKMLIKADQHHLDLTALPTPESTPTLQQKRKP 770
      : | :| | :| |:| |:| :| ||||| | ||
Db      652 EYQQNIDSPKLYSNLLTSRKELPPNGDTKSMVMDHRGQPPELAALPTPESTPVLHQKTLQ 711

Qy      771 SRGSREWERNQNINACTKDMPPMGSPVIPTDLPLRASPSHIPSVVVLPIITQQGYQHEY- 829
      : | : : : | |:| | || | ||| :|| | :
Db      712 AMKSHSEKAHGH--GASRKETPQFFPSPPPHSPL--SHGHIPSAIVLPNATHDYNTSFS 767

Qy      830 -----VDQP---KMSEVAQMALEDQAATLEYKTIKEHLSSKSPN----- 865
      :| | |: | || : :|| : |
Db      768 NSNAHKAEEKLQNIDHPLTKSSSKRDHRRSVDSRNTL--NDLLKHLNDPNSNPKAIMGDI 825

Qy      866 ---HGVNLVENLDSL---PPKVPQREASLGPPGASLSQTGLSKRLEMHHSSSY---GVDY 916
      | : : : |:| |||| |||| | :| : :||: : :
Db      826 QMAHQNLMLDPMGSMSEVPKVPNREASLYSPSTLPRNSPTKRVDVPTTPGVPMTSLER 885

Qy      917 KRSYPTNSLTRSHQATTLKRNTNSSNSSHLSRNQSFGRGD-NPPPAPQRVDSIQVHSSQ 975
      :| | || | : : : | || | || | | | :|| |
Db      886 QRGYHKNSSQR-HSISAMPK-NLNSPNGVLLSRQPSMNRGGYMPPTPTGAKVDYIQ----- 938

Qy      976 PSGQAVTVSRQPSLNAYNSLT-----RSGLKRTPSLKPDVPPKPSFAPLSTSMKP 1025
      | |:| |||: :| | |:| ||||| ||||| | :| :|
Db      939 --GTPVSVHLQPSLSRQSSYTSNGTLPRTLGLKRTPSLKPDVPPKPSFVPQTPSVRP 992

```

RESULT 12

Q8NFY3

```

ID   Q8NFY3          PRELIMINARY;          PRT;   1011 AA.
AC   Q8NFY3;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Semaphorin 6D isoform 1.
GN   SEMA6D.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RA   Qu X., Wei H., Zhai Y., Yu Y., Tang F., He F.;
RT   "Homo sapiens semaphorin 6D isoform 1 (SEMA6D.1) mRNA, complete cds.";
RL   Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF389430; AAM69453.1; -.
DR   InterPro; IPR001627; Sema.

```

DR Pfam; PF01403; Sema; 1.
DR SMART; SM00630; Sema; 1.
SQ SEQUENCE 1011 AA; 113289 MW; 9D6B8B3633941B89 CRC64;

Query Match 42.5%; Score 2314; DB 4; Length 1011;
Best Local Similarity 45.4%; Pred. No. 1.8e-179;
Matches 494; Conservative 155; Mismatches 292; Indels 148; Gaps 26;

```
Qy      1 MRSEALLLYFTLL---HFAGAGFPEDSEPISISHGNYTKQYPVFVGHKPGRNTTQRHRLD 57
      || | | | | ||| ||:: :|::| | | | :| | | | |
Db      1 MRVFLLCAYILLMVSQLRVASFPEDEPLNTVDYHYSRQYPVFRG-RPSGNESQ-HRLD 58

Qy     58 IQMIMIMNGTLYIAARDHIYTVDDIDTSHTEEIYCSKKLTWKSQADVDTCRMKGKHKDEC 117
      |::: : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     59 FQLMLKIRDITLYIAGRDQVYTVNLNEMPKTEVIPNKKLTWRSRQQDRENCAMKGKHKDEC 118

Qy    118 HNFIVKLLKKNDALFVCGTNAFNPSCRNYKMDTLEPFGDEFSGMARCPYDAKHANVALF 177
      | | | | | : : | | : | | | | | | | | | | | | | | | | | | | | | | |
Db    119 HNFIVKVFVRNDEMVFVCGTNAFNPSCRNYRSTLEYDGEEISGLARCPFDARQTNVALF 178

Qy    178 ADGKLYSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYFFFR 237
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    179 ADGKLYSATVADFLASDAVIYRSMGDGSALRTIKYDSKWIKEPHFLHAIEYGNVYFFFR 238

Qy    238 EIAVEYNTMGKVVFPRVAQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDSHFYFNILQ 297
      | | | | : | : | | : | | | | | | | | | | | | | | | | | | | | | |
Db    239 EIAVEHNNLGKAVYSRVARICKNDMGGSQRVLEKHWTSTFLKARLNCSVPGDSFFYFDVLQ 298

Qy    298 AVTDVIRINGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVP 357
      : | | : | | | | : | | | | | | | | | | | | | | | | | | | | | | |
Db    299 SITDIIQINGIPTVVGVFETTQLNSIPGSAVCAFSMDIEKVFKEQKTPDSVWTAVP 358

Qy    358 DERVPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVR 417
      : : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    359 EDKVPKPRPGCCAKHGLAEAYKTSIDFPDETLSFIKSHPLMDSAVPPIADEPWFETKTRVR 418

Qy    418 YRLTKIAVDTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGF-LNDSLFLLEEMSVYNSEK 476
      | | | | | : | | : | | | | | | | | | | | | | | | | | | | | | | |
Db    419 YRLTAISVDHSAGPYQNYTVIFVGSEAGMVLKVLAK--TSPFSLNDSVLLLEEIEAYNHAK 476

Qy    477 CSYDGVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRCERHGKCKKTCIASRDPYCGWI 536
      | | : | | | : : : | | | : | | | | | | | | | | | | | | | | | | |
Db    477 CSAENEEDKKVISLQLDKDHHALYVAFSSCIIRIPLSRCERYGSCCKKSCIASRDPYCGWL 536

Qy    537 KEGGACSHLSPNSRLT-----FEQDIERGNTDGLGDCHNSFVALNGHSSSL 582
      : | : | : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    537 SQ-GSCGRVTPGMLLLLTEDFFAFHNHSAEGYEQDTEFGNTAHLGDCHG----- 583

Qy    583 LPSTTTSDSTAQEGYESRGGMLDWKHLLDSPDSTDPLGAVSSHNDKKGVIRESYLKGH 642
      : | : : | : | | | | | | | | | | | | | | | | | | | | | | | | |
Db    584 -----VRWE--VQSGES----- 593

Qy    643 DQLVPVTLIAIAVILAFVMGAVFSGITVYCVCD-HRRKDVAVVQRKEKELTHSRRGSMSS 701
      : | : | : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    594 NQMVHNMVLITCVFAAFVLGAFIAGVAVYCYRDMFVRKNRKI--HKDAESAQSCTDSSGS 651

Qy    702 VTKLSGLFG---DTQSKDPKPEAILTPLMHNGKLATPGNTAKMLIKADQHHLDLTALPT 757
```



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      ||:||||      : |      | :      | :|      |:|      |:|      :| ||||
Db      652 FAKLNGLFDSVPKEYQQNIDSPKLYSNLLTSRKELPPNGDTKSMVMDHRGQPPELAALPT 711

Qy      758 PESTPTLQQKRKPSRGSREWERNQNLINACTKDMPPMGSPVIPTDLPLRASPSHIPSVVV 817
      ||||| | ||      : |      : : :      | |:|      | ||      | |||| :|
Db      712 PESTPVLHQKTLQAMKSHSEKAHGH--GASRKETPQFFPSSPPPHSPL--SHGHIPIAIV 767

Qy      818 LPITQQGYQHEY-----VDQP---KMSEVAQMALEDQAATLEYKTIKEHLS 860
      ||      | :      :| |      |:      | ||      : :||:
Db      768 LPNATHDYNTSFSNSNAHKAEEKKLQNIHPLTKSSSKRDHRSVDSRNTL--NDLLKHLN 825

Qy      861 SKSPN-----HGVNLVENLDSL---PPKVPQREASLGPPGASLSQTGLSKRLEM 906
      : |      | : : : | : |||| |||| | :| :      :|: : :
Db      826 DPNSNPKAIMGDIQMAHQNLMLDPMGSMSEVPPKVPNREASLYSPSTLPRNSPTKRVDV 885

Qy      907 HHSSSY---GVDYKRSYPTNSLTRSHQATTLKRNTNTSSNSSHLSRNQSFGRGD-NPPPA 962
      :      : : :| | || | | : : : | || | || | | || | |
Db      886 PTPPGVPMTSLERQRGYHKNSSQR-HSISAMPK-NLNSPNGVLLSRQPSMNRGGYMPPTPT 943

Qy      963 PQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLT-----RSGLKRTPSLKPDPVPPKPSF 1016
      :|| ||      | |:| ||||: :| |      |:||||||| ||||| |||||
Db      944 GAKVDYIQ-----GTPVSVHLQPSLSRQSSYTSNGTLPRTLGLKRTPSLKPDPVPPKPSF 996

Qy      1017 APLSTSMKP 1025
      | : | :|
Db      997 VPQTPSVRP 1005

```

RESULT 13

Q9P249

```

ID   Q9P249          PRELIMINARY;          PRT;  1022 AA.
AC   Q9P249;
DT   01-OCT-2000   (TrEMBLrel. 15, Created)
DT   01-OCT-2001   (TrEMBLrel. 18, Last sequence update)
DT   01-JUN-2003   (TrEMBLrel. 24, Last annotation update)
DE   Hypothetical protein KIAA1479 (Fragment).
GN   KIAA1479.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20277482; PubMed=10819331;
RA   Nagase T., Kikuno R., Ishikawa K., Hirosawa M., Ohara O.;
RT   "Prediction of the coding sequences of unidentified human
RT   genes.XVII.The complete sequences of 100 new cDNA clones from brain
RT   which code for large proteins in vitro.";
RL   DNA Res. 7:143-150(2000).
DR   EMBL; AB040912; BAA96003.2; -.
DR   GO; GO:0007275; P:development; IEA.
DR   InterPro; IPR003659; Plexin-like.
DR   InterPro; IPR001627; Sema.
DR   Pfam; PF01403; Sema; 1.
DR   SMART; SM00423; PSI; 1.
DR   SMART; SM00630; Sema; 1.
KW   Hypothetical protein.

```

FT NON TER 1 1
SQ SEQUENCE 1022 AA; 114372 MW; BE4FBD5EA02C69C4 CRC64;

Query Match 42.5%; Score 2314; DB 4; Length 1022;
Best Local Similarity 45.4%; Pred. No. 1.8e-179;
Matches 494; Conservative 155; Mismatches 292; Indels 148; Gaps 26;

```
QY      1 MRSEALLLYFTLL---HFAGAGFPEDSEPISISHGNYTKQYPVFVGHKPGRNTTQRHRLD 57
      || | | || ||| ||:: :|::| || | :| | :| |||
Db      12 MRVFLLCAYILLMVSQLRVSPFEDDEPLNTVDYHYSRQYPVFRG-RPSGNESQ-HRLD 69

QY      58 IQMIMIMNGTLYIAARDHIYTVDIDTSHTEEIYCSKKLTWKSQADVDTCRMKGKHKDEC 117
      |::: : |||| || :||::: | :|||:| || | :| |||||
Db      70 FQLMLKIRDTLYIAGRDQVYTVNLNEMPKTEVIPNKKLTWRSRQQDRENCAMKGKHKDEC 129

QY     118 HNFIVKLLKKNDDALFVCGTNAFNPSCRNYKMDTLEPFGDEFSGMARCPYDAKHANVALF 177
      ||||| : :||: :||| |||| || ||: || | :| ||:| ||:| :| ||||
Db     130 HNFIVKVFVRNDEMVFVCGTNAFNPSCRNYRLSTLEYDGEIISGLARCPFDARQTNVALF 189

QY     178 ADGKLYSATVTDFLAIDAVIYRSLGESPTLRVTKHDSKWLKEPYFVQAVDYGDIYFFFR 237
      ||||| ||| ||||| :| :||:| :||:| :||:| :| :| :| :| :|
Db     190 ADGKLYSATVADFLASDAVIYRSMGDGSALRTIKYDSKWIKEPHFLHAIEYGNVYFFFR 249

QY     238 EIAVEYNTMGKVVFPRVAQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDSHFYFNILQ 297
      ||||:| :|| | : ||::: ||||| ||||| ||||| ||||| |||:|
Db     250 EIAVEHNNLGKAVYSRVARICKNDMGGSQRVLEKHWTSTFLKARLNCSVPGDSFFYFDVLQ 309

QY     298 AVTDVIRINGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVP 357
      :||:| :|| | : | :| ||||| :| || || ||||| :|| | ||
Db     310 SITDIIQINGIPTVVGVTQNLNIPGSAVCAFSMDIEKVFKEGRFKEQKTPDSVWTAVP 369

QY     358 DERVPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVR 417
      ::||| ||| | | | :||:| :||:| ||| || | : || :| ||
Db     370 EDKVPKPRPGCCAKHGLAEAYKTSIDFPDETLSFIKSHPLMDSAVPPIADEPWFTKTRVR 429

QY     418 YRLTKIAVDTAAGPYQNHTVTVFLGSEKGIILKFLARIGNSGF-LNDSLFLLEMSVYNSEK 476
      |||| | :| :||| :||:| || :|| ||: | | ||| : ||| | | |
Db     430 YRLTAISVDHSAGPYQNYTVIFVGSEAGMVLKVLAK--TSPFSLNDSVLLEEIEAYNHAK 487

QY     477 CSYDGVEDKRIMGMQLDRASSSLYAFSTCVIKVPLGRGERHGKCKKTCIASRDPYCGWI 536
      || : |||:: :||: :||| :||| :||:| ||| :| ||||| :|
Db     488 CSAENEEDKKVISLQLDKDHHALYVAFSSCIIRIPLSRCERYGSCCKKSCIASRDPYCGWL 547

QY     537 KEGGACSHLSPNSRLT-----FEQDIERGNTDGLGDCHNSFVALNGHSSSL 582
      : | :| :| | : ||| | ||| ||||
Db     548 SQ-GSCGRVTPGMLLLTEDFFAFHNHSAEGYEQDTEFGNTAHLGDCHG----- 594

QY     583 LPSTTTSDSTAQEGYESRGGMLDWKHLSDPDSTDPLGAVSSHNHQDKKGVIRESYLKGH 642
      : | : | : |
Db     595 -----VRWE--VQSGES----- 604

QY     643 DQLVPVTLIAIAVILAFVMGAVFSGITVYCVCD-HRRKDVAVVQRKEKELTHSRRGSMSS 701
      :| :| :| | ||:| :| || | ||: : | :| | | |
Db     605 NQMVMHNVLITCVFAAFVLGAFIAGVAVYCYRDMFVRKNRKI--HKDAESAQSCTDSSGS 662

QY     702 VTKLSGLFG----DTQSKDPKPEAILTPLMHNGKLATPGNTAKMLIKADQHHLDTALPT 757
      ||:| | : | : | :| | :| :| |||
```

Db 663 FAKLNGLFDSPVKEYQQNIDSPKLYSNLLTSRKELPPNGDTKSMVMDHRGQPPELAALPT 722

Qy 758 PESTPTLQQRKPSRGSREWERNQNLINACTKDMPPMGSPVIPTDLPLRASPSHIPSVVV 817
 ||||| | || : | : : : | | : | | || | |||| : |

Db 723 PESTPVLHQKTLQAMKSHSEKAHGH--GASRKETPQFFPSSPPPHSPL--SHGHIPSAIV 778

Qy 818 LPITQQGYQHEY-----VDQP---KMSEVAQMALEDQAATLEYKTIKEHLS 860
 || | : : | | | : | || : : || :

Db 779 LPNATHDYNTSFSNSNAHKAEEKLQNIHPLTKSSSKRDHRRSVDSRNTL--NDLLKHLN 836

Qy 861 SKSPN-----HGVNLVENLDSL---PPKVPQREASLGPPGASLSQTGLSKRLEM 906
 : | | : : : | : ||||| ||||| | : : | : : || : :

Db 837 DPNNSPKAIMGDIQMAHQNLMLDPMGSMSEVPPKVPNREASLYSPSTLPRNSPTKRVDV 896

Qy 907 HHSSSY---GVDYKRSYPTNSLTRSHQATT LKRNTNTSSNSSHLSRNQSFGRGD-NPPPA 962
 : : : | | || | | : : : | || | || | | || | |

Db 897 PTPGVPMTSLERQRGYHKNSSQR-HSISAMPK-NLNSPNGVLLSRQPSMNRGGYMPPTPT 954

Qy 963 PQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLT-----RSLKRTPSLKPDVPPKPSF 1016
 : || || | | : | |||| : : | | | : ||||| ||||| |||||

Db 955 GAKVDYIQ-----GTPVSVHLQPSLSRQSSYTSNGTLPTGLKRTPSLKPDVPPKPSF 1007

Qy 1017 APLSTSMKP 1025
 | : | : |

Db 1008 VPQTPSVRP 1016

RESULT 14

Q80TD0

ID Q80TD0 PRELIMINARY; PRT; 1009 AA.

AC Q80TD0;

DT 01-JUN-2003 (TrEMBLrel. 24, Created)

DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE MKIAA1479 protein (Fragment).

GN MKIAA1479.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Brain;

RX MEDLINE=22579291; PubMed=12693553;

RA Okazaki N., Kikuno R., Ohara R., Inamoto S., Aizawa H., Yuasa S.,

RA Nakajima D., Nagase T., Ohara O., Koga H.;

RT "Prediction of the coding sequences of mouse homologues of KIAA gene:

RT II. The complete nucleotide sequences of 400 mouse KIAA-homologous

RT cDNAs identified by screening of terminal sequences of cDNA clones

RT randomly sampled from size-fractionated libraries.";

RL DNA Res. 10:35-48(2003).

DR EMBL; AK122515; BAC65797.1; -.

DR InterPro; IPR001627; Sema.

DR Pfam; PF01403; Sema; 1.

DR SMART; SM00630; Sema; 1.

FT NON_TER 1 1

SQ SEQUENCE 1009 AA; 112808 MW; 7509F0B67332316B CRC64;

Query Match 42.4%; Score 2309.5; DB 11; Length 1009;
 Best Local Similarity 46.1%; Pred. No. 4.1e-179;
 Matches 497; Conservative 154; Mismatches 280; Indels 147; Gaps 30;

Qy	6	LLLYFTLL-----HFAGAGFPEDSEPISISHGNYTKQYPVFVGHKPGRNNTQRRHRLDIQM	60
		: : :: : :: : : :	
Db	15	LLWFCVLFLLSRLRAVSFPEDDEPLNTVDYHYSRQYPVFRG-RPSGNESQ-HRLDFQL	72
Qy	61	IMIMNGTLYIAARDHIYTVDIDTSHTEEIYCSKKLTWKSQRQADVDTCRMKGKHKDECHNF	120
		:: : : ::: : : :	
Db	73	MLKIRDTLYIAGRDQVYTVNLNEIPQTEVIPSKKLTWRSRQQDRENCAMKGKHKDECHNF	132
Qy	121	IKVLLKKND DALFVCGTNAFNPSCRNYKMDTLEPFGEDEFSGMARCPYDAKHANVALFADG	180
		: : : : : : : : :	
Db	133	IKVFVPRNDEMVFVCGTNAFNPMCRYRLRTLEYDGEIISGLARCPFDARQTNVALFADG	192
Qy	181	KLYSATVTDFLAIDAVIYRSLGESPTLRVTVKHDSKWLKEPYFVQAVDYGDIYFFFREIA	240
		: : : : : : : : :	
Db	193	KLYSATVADFLASDAVIYRSMGDGSALRTIKYDSKWIKEPHFLHAIEYGNVYVFFFREIA	252
Qy	241	VEYNTMGKVVFPRAVQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDSHFYFNILQAVT	300
		: : : ::: : ::	
Db	253	VEHNNLGKAVYSRVARICKNDMGGSQRVLEKHWTSFLKARLNCSVPGDSFFYFDVLQSIT	312
Qy	301	DVIRINGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVPDER	360
		: : : : : : :::	
Db	313	DIIQINGIPTVVGVTTLQNSIPGSAVCAFSMDIEKVFKGRFKEQKTPDSVWTAVPEDK	372
Qy	361	VPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRL	420
		: : : :	
Db	373	VPKPRPGCCAKHGLAEAYKTSIDFPDDTLAFIKSHPLMDSAVPPIADEPWFTKTRVRYRL	432
Qy	421	TKIAVDTAAGPYQNHTVTVFLGSEKGIILKFLARIGNSGF-LNDSLFLLEMSVYNSEKCSY	479
		: : : :: : : :	
Db	433	TAIEVDRSAGPYQNYTVIFVGSEAGVVLKVLAK--TSPFSLNDSVLLEEIEAYNPAKCSA	490
Qy	480	DGVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRCERHGKCKKTCIASRDPYCGWIKEG	539
		: ::: : : : :: : : : :	
Db	491	ESEEDRKVVSLLQDKDHHALYVAFSSCVVRIPLSRCERYGSCCKKSCIASRDPYCGWLSQ-	549
Qy	540	GACSHLS----PNSRLTFEQDIERGNTDGLGDCHNSFVALNGHSSSLPSTTTSDSTAQE	595
		: : :	
Db	550	GVCERVTLGMLPGG---YEQDTEYGNHTAHLGDCHG-----	581
Qy	596	GYESRGMLDWKHLSDSPDSTDPLGAVSSHNHQDKKGVIRESYLKGHDLVPVTLIAIAV	655
		: : : : : : : :	
Db	582	-----VRWE--VQSGES-----NQMVHNVLITCV	604
Qy	656	ILAFVMGAVFSGITVYCVCD-HRRKDVAVVQRKEKELTHSRRGSMSSVTKLSGLFGDTQS	714
		: : : : : : :	
Db	605	FAAFVLGAFIAGVAVYCYRDMFVRKNRKI--HKDAESAQSCDSSSGSFAKLNGLF-DSPV	661
Qy	715	KDPKPEAILTPLMHNGKLAT----PGNTAKMLIKADQHHL--DLTALPTPESTPTLQOKR	768
		: : : : :: : : :	
Db	662	KEYQ-QNIDSPKLYSNLLTSRKELPPNTDTKSMAVDHRGQPPELAALPTPESTPVLHQKT	720

Qy 122 KVLKKNDALFVCGTNAFNPSCRNYKMDTLEPFGDEFSGMARCPYDAKHANVALFADGK 181
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 61 KVLKKNDALFVCGTNAFNPSCRNYKMDTLEPFGDEFSGMARCPYDAKHANVALFADGK 120

Qy 182 LYSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYFFFREIAV 241
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 121 LYSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYFFFREIAV 180

Qy 242 EYNTMGKVVFPRAQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDSHFYFNILQAVTD 301
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 181 EYNTMGKVVFPRAQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDSHFYFNILQAVTD 240

Qy 302 VIRINGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVDERV 361
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 241 VIRINGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVDERV 300

Qy 362 PKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRLT 421
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 301 PKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRLT 360

Qy 422 KIAVDTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLNDSLFLLEEMSVYNSEK 476
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 361 KIAVDTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLNDSLFLLEEMSVYNSEK 415

Search completed: March 24, 2004, 13:16:25
 Job time : 75.9691 secs

OM protein - protein search, using sw model

Run on: March 24, 2004, 13:07:38 ; Search time 20.5626 Seconds
(without alignments)
2608.241 Million cell updates/sec

Title: US-09-856-681A-2
Perfect score: 5450
Sequence: 1 MRSEALLLYFTLLHFAGAGF.....PPKPSFAPLSTSMKPNDACT 1030

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Query	Match	Length	DB	ID	Description
1	5450	100.0	1030	1	SM6A_HUMAN	Q9h2e6	homo sapien
2	4346.5	79.8	888	1	SM6A_MOUSE	O35464	mus musculu
3	2013.5	36.9	888	1	SM6B_HUMAN	Q9h3t3	homo sapien
4	1997	36.6	887	1	SM6B_RAT	O70141	rattus norv
5	1995	36.6	886	1	SM6B_MOUSE	O54951	mus musculu
6	1515.5	27.8	930	1	SM6C_HUMAN	Q9h3t2	homo sapien
7	1493.5	27.4	931	1	SM6C_MOUSE	Q9wtm3	mus musculu
8	1491	27.4	960	1	SM6C_RAT	Q9wtl3	rattus norv
9	971.5	17.8	730	1	SM1A_SCHAM	Q26473	schistocerc
10	932.5	17.1	771	1	SM1A_DROME	Q24322	drosophila
11	858	15.7	772	1	SM3A_RAT	Q63548	rattus norv
12	853	15.7	772	1	SM3A_MOUSE	O08665	mus musculu
13	852.5	15.6	771	1	SM3A_HUMAN	Q14563	homo sapien
14	845	15.5	712	1	SM1A_TRICF	Q26972	tribolium c
15	845	15.5	778	1	SZ1B_BRARE	Q9w686	brachydanio
16	845	15.5	860	1	SZ1A_BRARE	Q9w7j1	brachydanio
17	839.5	15.4	772	1	SM3A_CHICK	Q90607	gallus gall

18	830	15.2	1074	1	SM5A_HUMAN	Q13591	homo sapien
19	826	15.2	749	1	SM3B_HUMAN	Q13214	homo sapien
20	825.5	15.1	1077	1	SM5A_MOUSE	Q62217	mus musculu
21	803	14.7	748	1	SM3B_MOUSE	Q62177	mus musculu
22	803	14.7	764	1	SMZ2_BRARE	Q9w6g6	brachydanio
23	797	14.6	777	1	SM3D_HUMAN	O95025	homo sapien
24	793.5	14.6	761	1	SM3D_CHICK	Q90663	gallus gall
25	789	14.5	712	1	SM1A_CAEEL	Q17330	caenorhabdi
26	770.5	14.1	1093	1	SM5B_HUMAN	Q9p283	homo sapien
27	766	14.1	1093	1	SM5B_MOUSE	Q60519	mus musculu
28	762.5	14.0	706	1	SM2A_DROME	Q24323	drosophila
29	762	14.0	775	1	SM3E_HUMAN	O15041	homo sapien
30	752	13.8	751	1	SM3C_CHICK	O42236	gallus gall
31	751	13.8	861	1	SM4D_MOUSE	O09126	mus musculu
32	750.5	13.8	697	1	SM2A_SCHGR	Q9xzc8	schistocerc
33	749	13.7	785	1	SM3F_HUMAN	Q13275	homo sapien
34	744.5	13.7	785	1	SM3F_MOUSE	O88632	mus musculu
35	739	13.6	775	1	SM3E_MOUSE	P70275	mus musculu
36	737	13.5	751	1	SM3C_MOUSE	Q62181	mus musculu
37	735.5	13.5	862	1	SM4D_HUMAN	Q92854	homo sapien
38	733.5	13.5	785	1	SM3E_CHICK	O42237	gallus gall
39	733	13.4	751	1	SM3C_HUMAN	Q99985	homo sapien
40	700.5	12.9	766	1	SMZ7_BRARE	Q9yhx4	brachydanio
41	692	12.7	834	1	SM4C_MOUSE	Q64151	mus musculu
42	681	12.5	832	1	SM4B_HUMAN	Q9npr2	homo sapien
43	671	12.3	761	1	SM4A_HUMAN	Q9h3s1	homo sapien
44	664	12.2	776	1	SM4F_RAT	Q9z143	rattus norv
45	658	12.1	777	1	SM4F_MOUSE	Q9z123	mus musculu

ALIGNMENTS

RESULT 1

SM6A_HUMAN

ID SM6A_HUMAN STANDARD; PRT; 1030 AA.

AC Q9H2E6; Q9P2H9;

DT 10-OCT-2003 (Rel. 42, Created)

DT 10-OCT-2003 (Rel. 42, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Semaphorin 6A precursor (Semaphorin VIA) (Sema VIA) (Semaphorin 6A-1)

DE (SEMA6A-1).

GN SEMA6A OR KIAA1368.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A., AND INTERACTION WITH EVL.

RX MEDLINE=20564339; PubMed=10993894;

RA Klostermann A., Lutz B., Gertler F., Behl C.;

RT "The orthologous human and murine semaphorin 6A-1 proteins

RT (SEMA6A-1/Sema6A-1) bind to the enabled/vasodilator-stimulated

RT phosphoprotein-like protein (EVL) via a novel carboxyl-terminal

RT zyxin-like domain.";

RL J. Biol. Chem. 275:39647-39653(2000).

RN [2]

RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=20181126; PubMed=10718198;
 RA Nagase T., Kikuno R., Ishikawa K.-I., Hirose M., Ohara O.;
 RT "Prediction of the coding sequences of unidentified human genes. XVI.
 RT The complete sequences of 150 new cDNA clones from brain which code
 RT for large proteins in vitro.";
 RL DNA Res. 7:65-73(2000).
 CC -!- FUNCTION: Can act as repulsive axon guidance cues. May play a role
 CC in channeling sympathetic axons into the sympathetic chains and
 CC controlling the temporal sequence of sympathetic target
 CC innervation (By similarity).
 CC -!- SUBUNIT: Active as a homodimer or oligomer. Interacts with EVL.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=Q9H2E6-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=Q9H2E6-2; Sequence=VSP_007113;
 CC Note=No experimental confirmation available;
 CC -!- SIMILARITY: Belongs to the semaphorin family.
 CC -!- SIMILARITY: Contains 1 Sema domain.
 CC -----
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 CC -----
 DR EMBL; AF279656; AAG29378.1; -.
 DR EMBL; AB037789; BAA92606.1; ALT_INIT.
 DR Genew; HGNC:10738; SEMA6A.
 DR MIM; 605885; -.
 DR GO; GO:0030424; C:axon; NAS.
 DR GO; GO:0016021; C:integral to membrane; NAS.
 DR GO; GO:0008580; F:cytoskeletal regulator activity; NAS.
 DR GO; GO:0005515; F:protein binding; IPI.
 DR GO; GO:0006915; P:apoptosis; NAS.
 DR GO; GO:0007411; P:axon guidance; NAS.
 DR GO; GO:0007166; P:cell surface receptor linked signal transdu. . .; NAS.
 DR GO; GO:0007399; P:neurogenesis; NAS.
 DR InterPro; IPR003659; Plexin-like.
 DR InterPro; IPR001627; Sema.
 DR Pfam; PF01403; Sema; 1.
 DR SMART; SM00423; PSI; 1.
 DR SMART; SM00630; Sema; 1.
 KW Signal; Transmembrane; Multigene family; Neurogenesis; Glycoprotein;
 KW Developmental protein; Alternative splicing.
 FT SIGNAL 1 18 POTENTIAL.
 FT CHAIN 19 1030 SEMAPHORIN 6A.
 FT DOMAIN 19 649 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 650 670 POTENTIAL.
 FT DOMAIN 671 1030 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 56 491 SEMA.

FT	DOMAIN	792	819	PRO-RICH.
FT	CARBOHYD	33	33	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	49	49	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	65	65	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	282	282	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	434	434	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	461	461	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	VARSP LIC	576	576	N -> NDISTPLPDNEMSYNTVY (in isoform 2).
FT				/FTId=VSP_007113.
SQ	SEQUENCE	1030 AA;	114368 MW;	A57B79C10AEC4B34 CRC64;

Query Match 100.0%; Score 5450; DB 1; Length 1030;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1030; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MRSEALLLYFTLLHFAGAGFPEDSEPI	ISHGNYTKQYPVFVGHKPGRNTTQRHRLDIQM	60
Db	1	MRSEALLLYFTLLHFAGAGFPEDSEPI	ISHGNYTKQYPVFVGHKPGRNTTQRHRLDIQM	60
Qy	61	IMIMNGTLYIAARDHIYTVDIDTSHTEEIYCSKKLTWKS	RQADVDTCRMKGKHKDECHNF	120
Db	61	IMIMNGTLYIAARDHIYTVDIDTSHTEEIYCSKKLTWKS	RQADVDTCRMKGKHKDECHNF	120
Qy	121	IKVLLKKND DALFVCGTNAFNPSCRNYKMDTLEPFGDEFSG	MARCPYDAKHANVALFADG	180
Db	121	IKVLLKKND DALFVCGTNAFNPSCRNYKMDTLEPFGDEFSG	MARCPYDAKHANVALFADG	180
Qy	181	KLYSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQ	AVDYGDIYFFFREIA	240
Db	181	KLYSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQ	AVDYGDIYFFFREIA	240
Qy	241	VEYNTMGKVVFPRVAQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDSHFYFNILQAVT	300	
Db	241	VEYNTMGKVVFPRVAQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDSHFYFNILQAVT	300	
Qy	301	DVIRINGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVPDER	360	
Db	301	DVIRINGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVPDER	360	
Qy	361	VPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRL	420	
Db	361	VPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRL	420	
Qy	421	TKIAVDTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLNDSLFLEEMSVYNSEKCSYD	480	
Db	421	TKIAVDTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLNDSLFLEEMSVYNSEKCSYD	480	
Qy	481	GVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRRCERHKGCKKTCIASRDPYCGWIKEGG	540	
Db	481	GVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRRCERHKGCKKTCIASRDPYCGWIKEGG	540	
Qy	541	ACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALNGHSSSLPSTTTSDSTAQEGYESR	600	
Db	541	ACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALNGHSSSLPSTTTSDSTAQEGYESR	600	
Qy	601	GGMLDWKHL L D S P D S T D P L G A V S S H N H Q D K K G V I R E S Y L K G H D Q L V P V T L L A I A V I L A F V	660	

Db	601	GGMLDWKHLLDSPDSTDPLGAVSSHNHQDKKGVIRESYLKGHDLVQVPTLLAIAVILAFV	660
Qy	661	MGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRGSMSSVTKLSGLFGDTQSKDPKPE	720
Db	661	MGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRGSMSSVTKLSGLFGDTQSKDPKPE	720
Qy	721	AILTPLMHNGKLATPGNTAKMLIKADQHHLDTALPTPESTPTLQQKRKPSRGSREWERN	780
Db	721	AILTPLMHNGKLATPGNTAKMLIKADQHHLDTALPTPESTPTLQQKRKPSRGSREWERN	780
Qy	781	QNLINACTKDMPPMGSPVIPTDLPLRASPSHIPSVVVLPITQQGYQHEYVDQPKMSEVAQ	840
Db	781	QNLINACTKDMPPMGSPVIPTDLPLRASPSHIPSVVVLPITQQGYQHEYVDQPKMSEVAQ	840
Qy	841	MALEDQAATLEYKTIKEHLSSKSPNHGVNLVENLDSLPPKVPQREASLGPPGASLSQTGL	900
Db	841	MALEDQAATLEYKTIKEHLSSKSPNHGVNLVENLDSLPPKVPQREASLGPPGASLSQTGL	900
Qy	901	SKRLEMHHSSSYGVDYKRSYPTNSLTRSHQATTLKRNNTNSSNSSHLSRNQSFGRGDNPP	960
Db	901	SKRLEMHHSSSYGVDYKRSYPTNSLTRSHQATTLKRNNTNSSNSSHLSRNQSFGRGDNPP	960
Qy	961	PAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRTPSLKPDPVPPKPSFAPLS	1020
Db	961	PAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRTPSLKPDPVPPKPSFAPLS	1020
Qy	1021	TSMKPNDACT	1030
Db	1021	TSMKPNDACT	1030

RESULT 2

SM6A_MOUSE

ID SM6A_MOUSE STANDARD; PRT; 888 AA.

AC O35464;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Semaphorin 6A precursor (Semaphorin VIA) (Sema VIA) (Semaphorin 6A-1)

DE (SEMA6A-1) (Semaphorin Q) (Sema Q).

GN SEMA6A OR SEMAQ.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=97348468; PubMed=9204478;

RA Zhou L., White F.A., Lentz S.I., Wright D.E., Fisher D.A.,

RA Snider W.D.;

RT "Cloning and expression of a novel murine semaphorin with structural

RT similarity to insect semaphorin I.";

RL Mol. Cell. Neurosci. 9:26-41(1997).

RN [2]

RP INTERACTION WITH EVL.

RX MEDLINE=20564339; PubMed=10993894;

RA Klostermann A., Lutz B., Gertler F., Behl C.;

RT "The orthologous human and murine semaphorin 6A-1 proteins
RT (SEMA6A-1/Sema6A-1) bind to the enabled/vasodilator-stimulated
RT phosphoprotein-like protein (EVL) via a novel carboxyl-terminal
RT zyxin-like domain.";
RL J. Biol. Chem. 275:39647-39653(2000).
CC -!- FUNCTION: Can act as repulsive axon guidance cues. May play a role
CC in channeling sympathetic axons into the sympathetic chains and
CC controlling the temporal sequence of sympathetic target
CC innervation.
CC -!- SUBUNIT: Active as a homodimer or oligomer. Interacts with EVL.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: Particularly high levels in spinal cord,
CC cerebellum, metencephalon, superior and inferior colliculus,
CC diencephalon, olfactory bulb and eye.
CC -!- DEVELOPMENTAL STAGE: Temporally and spatially regulated during
CC development.
CC -!- SIMILARITY: Belongs to the semaphorin family.
CC -!- SIMILARITY: Contains 1 Sema domain.
CC -----
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CC -----
DR EMBL; AF030430; AAB86408.1; -.
DR MGD; MGI:1203727; Sema6a.
DR GO; GO:0030424; C:axon; NAS.
DR GO; GO:0016020; C:membrane; NAS.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0006915; P:apoptosis; NAS.
DR GO; GO:0007411; P:axon guidance; NAS.
DR InterPro; IPR003659; Plexin-like.
DR InterPro; IPR001627; Sema.
DR Pfam; PF01403; Sema; 1.
DR SMART; SM00423; PSI; 1.
DR SMART; SM00630; Sema; 1.
KW Signal; Transmembrane; Multigene family; Neurogenesis; Glycoprotein;
KW Developmental protein.
FT SIGNAL 1 18 POTENTIAL.
FT CHAIN 19 888 SEMAPHORIN 6A.
FT DOMAIN 19 649 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 650 670 POTENTIAL.
FT DOMAIN 671 888 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 56 491 SEMA.
FT DOMAIN 792 819 PRO-RICH.
FT CARBOHYD 33 33 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 49 49 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 65 65 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 282 282 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 434 434 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 461 461 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 888 AA; 99075 MW; C7094FC2BB345C57 CRC64;

Query Match

79.8%; Score 4346.5; DB 1; Length 888;


```

Db      781 QNIINACTKDMPPMGSPVIPTDLPLRASPSHIPSVVVLPIITQQGYQHEYVDQPKMSEVVA 840
Qy      840 QMALEDQAATLEYKTIKEHLSSKS 863
        |||||:|
Db      841 QMALEDQAATLEYKTIKEHLSSES 864

```

RESULT 3

SM6B_HUMAN

```

ID      SM6B_HUMAN      STANDARD;      PRT;      888 AA.
AC      Q9H3T3; Q9NRK9;
DT      16-OCT-2001 (Rel. 40, Created)
DT      16-OCT-2001 (Rel. 40, Last sequence update)
DT      10-OCT-2003 (Rel. 42, Last annotation update)
DE      Semaphorin 6B precursor (Semaphorin Z) (Sema Z).
GN      SEMA6B OR SEMAZ.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A. (ISOFORM 1).
RC      TISSUE=Brain;
RA      Kimura T., Ishida H.;
RL      Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
RN      [2]
RP      SEQUENCE FROM N.A. (ISOFORM 2).
RX      MEDLINE=21248680; PubMed=11350127;
RA      Correa R.G., Sasahara R.M., Bengtson M.H., Katayama M.L.H.,
RA      Salim A.C.M., Brentani M.M., Sogayar M.C., de Souza S.J.,
RA      Simpson A.J.G.;
RT      "Human semaphorin 6b.";
RL      Genomics 73:343-348(2001).
CC      -!- FUNCTION: MAY PLAY A ROLE IN BOTH PERIPHERAL AND CENTRAL NERVOUS
CC      SYSTEM DEVELOPMENT (BY SIMILARITY).
CC      -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC      -!- ALTERNATIVE PRODUCTS:
CC      Event=Alternative splicing; Named isoforms=2;
CC      Comment=Additional isoforms seem to exist;
CC      Name=1;
CC      IsoId=Q9H3T3-1; Sequence=Displayed;
CC      Name=2; Synonyms=6B.1;
CC      IsoId=Q9H3T3-2; Sequence=VSP_006044, VSP_006045;
CC      -!- SIMILARITY: Belongs to the semaphorin family.
CC      -!- SIMILARITY: Contains 1 Sema domain.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; AB022433; BAB20669.1; -.
DR      EMBL; AF216389; AAF87661.1; -.
DR      Genew; HGNC:10739; SEMA6B.

```


Qy	60	MIMIMNGTLYIAARDHIYTVDIDTSHTEEIYCSKCLTWKSRQADVDTCRMKGKHKDECHN	119
Db	70	RVLVRNRTLFIFGDRDNLQVELEPSTSTELRYQRKLTWRSNPSDIDVCRMKGKQEGECRN	129
Qy	120	FIKVLKKKNDALFVCGTNAFNPSCRNYKMDTLEPFGDEFSGMARCPYDAKHANVALFAD	179
Db	130	FVKVLLLRDESTLFVCGSNAFNPICANYSMDTLQLLGDNISGMARCPYDPKHANVALFSD	189
Qy	180	GKLYSATVTDFLAIDAVIYRSLGESPTLRITVKHDSKWLKEPYFVQAVDYGDYIYFFFREI	239
Db	190	GMLFTATVTDFLAIDAVIYRSLGDRPTLRITVKHDSKWFKEPYFVHAVEWGSHVYFFFREI	249
Qy	240	AVEYNTMGKVVFPRVAQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDSHFYFENILQAV	299
Db	250	AMEFNYLEKVVSRRVARVCKNDVGGSPRVLEKQWTSFLKARLNCSVPGDSHFYFENVLQAV	309
Qy	300	TDVIRINGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVPDE	359
Db	310	TGVVSLGGRPVILAVFSTPSNSIPGSAVCAFDMNQVAAVFEGRFREQKSPESIWTVPED	369
Qy	360	RVPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYS	419
Db	370	QVPRPRPGCCAAPGM--QYNASNALPDEILNFVKTHPLMDEAVPSLGHSPWIVRTLIRHQ	427
Qy	420	LTKIAVDTAAGPYQNHTVVFLGSEKGIILKFLAR--IGNSGFLNDSLFLLEEMSVYNSEK	477
Db	428	LTRVAVDVGAGPWGNQITIVFLGSEVGTVLKFLVKPNASVSGTTGPSIFLEEFETYRPDC	487
Qy	478	---SYDGVEDKRIMGQLDRASSSLYAFSTCVIKVPLGRGERHGKCKKTCIASRDPYCG	534
Db	488	GRSSSAGEWQRLLSLELDAASGGLLAAPRCVVRVPVARCQLYSGCMKNCIGSQDPYCG	547
Qy	535	WIKEGGACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALNGHSSSLPSTTTSDSTAQ	594
Db	548	WAPD-GSCIFLRPGTSATFEQDVSGASTSGLGDC-----	580
Qy	595	EGYESRGGMLDWKHLSDSPDSTDPLGAVSSHNHQQKGVIRESYLKGHDLVPVTLAIA	654
Db	581	-----TGLLRASLSDDRAGLVSVNLLVTS	604
Qy	655	VILAFVMGAVFSGITV-YCVC DHRRKDVA VVQRKEKE--LTHSRSGSMSSVTKL-----	705
Db	605	SVAAFVVGAVVSGFSGVGFVGLRERRELA--RRKDKEAILAHGGSEAVLSVSRLGERRG	662
Qy	706	--SGLFGDTQSKDPKPEAILTPLMHNGKLATPGNTAKMLIKADQHHLDTALPTPESTPT	763
Db	663	GTGGRGGAGGGPGGPPEALLAPLMQNGW-----TKAALLHGGPHDLDSGLLPTEQTP-	715
Qy	764	LQQKRKPSR-----GSREWERNQNLINACTK-----DMPPMGSPVIPTD--	802
Db	716	LPQKRLPTTHPHAHALGPRAWDHSHALLSASASTSLLLLAHTRAPEQPP-----VPTESG	770
Qy	803	-----LPLRASPSHIPSVVVLPIITQQGYQHEYVDQPKMSEVAQMALEDQAATLEYKTIK	856
Db	771	PESRLCAPRSCRAHPGDFPLTP-----HASPDRRRVVSAPTGPLDSSSVG-----	816
Qy	857	EHLSSKSPNHGVNLVENLDSLIP-PKVPQREASL-----GPPGASLSQTGLSKRLEMHHS	909

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      | | | | | : | | | | | : | |
Db      817 -----DDLPGWSPPATSSLRRPGPHGPPTAALRRT-----HT 849

Qy      910 SSYGV DYKRSYPTNSLTRSHQATTLKRNTNTSSNSSHLSRNQSFGRGD-NPPAP 963
      : | : | | : | | : | |
Db      850 FNSG----EARPGGHRPRRHA-----PADSTHL---LPCGTGERTAPPVP 887

```

RESULT 5

SM6B_MOUSE

```

ID      SM6B_MOUSE      STANDARD;      PRT;      886 AA.
AC      O54951;
DT      30-MAY-2000 (Rel. 39, Created)
DT      30-MAY-2000 (Rel. 39, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DE      Semaphorin 6B precursor (Semaphorin VIB) (Sema VIB) (Semaphorin N)
DE      (Sema N).
GN      SEMA6B OR SEMAN.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=98027184; PubMed=9361278;
RA      Eckhardt F., Behar O., Calautti E., Yonezawa K., Nishimoto I.,
RA      Fishman M.C.;
RT      "A novel transmembrane semaphorin can bind c-src.";
RL      Mol. Cell. Neurosci. 9:409-419(1997).
CC      -!- SUBUNIT: HOMODIMER. BINDS SPECIFICALLY THE SH3 DOMAIN OF THE
CC      PROTOONCOGENE C-SRC.
CC      -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC      -!- TISSUE SPECIFICITY: During development it is expressed in
CC      subregions of the nervous system and is particularly prominent in
CC      muscle. In adulthood, it is expressed ubiquitously.
CC      -!- SIMILARITY: Belongs to the semaphorin family.
CC      -!- SIMILARITY: Contains 1 Sema domain.
CC      -----
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CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; AF036585; AAC00493.1; -.
DR      MGD; MGI:1202889; Sema6b.
DR      InterPro; IPR003659; Plexin-like.
DR      InterPro; IPR001627; Sema.
DR      Pfam; PF01403; Sema; 1.
DR      SMART; SM00423; PSI; 1.
DR      SMART; SM00630; Sema; 1.
KW      Signal; Transmembrane; Multigene family; Neurogenesis; Glycoprotein;
KW      Developmental protein.
FT      SIGNAL      1      26      POTENTIAL.
FT      CHAIN      27      886      SEMAPHORIN 6B.

```

FT	DOMAIN	27	605	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	606	626	POTENTIAL.
FT	DOMAIN	627	886	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	239	549	SEMA.
FT	DOMAIN	751	754	POLY-LEU.
FT	CARBOHYD	75	75	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	156	156	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	292	292	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	387	387	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	442	442	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	463	463	N-LINKED (GLCNAC. . .) (POTENTIAL).
SO	SEQUENCE	886 AA;	95466 MW;	E5F56D125CDA574D CRC64;

Qy	8	LYFTLLHFAGAG---FPEDSEPI SISHGNYTKQYPVFGHKPGRNTTQR--HRLDIQMIM	62
Db	13	LSFFLLLLLLGVTYGLFPPEEPPLSVAPRDYLSHYPVFVGSGPGRLTAAEGAEDLNIQRVL	72
Qy	63	IMNGTLYIAARDHIYTVDIDTSHTEEIYCSKKLTWKSQADVDTCRMKGKHKDECHNFIK	122
Db	73	RVNRTLFIGDRDONLYQVELEPSTSTELRYQRKLTWRSNPDSIDVCRMKGKQEGECRNFVK	132
Qy	123	VLLKKND DALFVCGTNAFNPSCRNYKMDTLEPFGDEFSGMARCPYDAKHANVALFADGKL	182
Db	133	VLLLRDESTLFVCGSNAFNPICANYSM DTLQLLGDSISGMARCPYDPKHANVALFSDGML	192
Qy	183	YSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYFFFFREIAVE	242
Db	193	FTATVTDFLAIDAVIYRSLGDRPTLRTVKHDSKWFKEPYFVHAVEWGS HVYFFFFREIAME	252
Qy	243	YNTMGKVVFPRVAQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPGD SHFYFNILQAVTDV	302
Db	253	FNYLEKVVS RVARVCKNDVGGSPRVLEKQWTSFLKARLNCSVPGD SHFYFNVLQAVTGV	312
Qy	303	IRINGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVPDERVP	362
Db	313	VSLGGRPVILAVFSTPSNSIPGSAVCAFD MNQVAAVFEGRFREQKSPESIWTPVPEDQVP	372
Qy	363	KPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRLTK	422
Db	373	RPRPGCCAAPGM--QYNASSALPDEILNFVKTHPLMDEAVPSLGHSPWIVRTL MRHQ LTR	430
Qy	423	IAVDTAAGPYQNHTVVFLGSEKGIILKFLAR--IGNSGFLNDSL FLEEMSVYNSEKC---	477
Db	431	VAVDVGAGPWGNQTIVFLGSEAGTVLKLFLVKPNASVSGTTGPSIFLEEFETYRPDRCGRP	490
Qy	478	SYDGVEDKRIMGMLDRASSSLYVAFSTCVIKVPLGRCERHGKCKKTCIASRDPYCGWIK	537
Db	491	SSAGEWGQRLLSLELDAASGGLLA AFPRCVVRVPVARCQLYSGCMKN CIGSQDPYCGWAP	550
Qy	538	EGGACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALNGHSSSLPSTTTSDSTAQEGY	597
Db	551	D-GSCIFLRPGTSATFEQDVSGASTSGLGDC-----	580

Qy 598 ESRGGLDWKHLLDSPDSTDPLGAVSSHNDKKGVIRESYLKGHDQLVPVTLIAIVIL 657
 Db 581 -----TGLLRASLSDDRAGLVSVNLLVTSSVA 607
 Qy 658 AFVMGAVFSGITV-YCVC DHRRKDVAVVQRKEKE--LTHSRRGSMSSVTKL SGLFGDTQS 714
 Db 608 AFVVGVAVVSGFVGVFWGLRERRELA--RRKDKEAILAHGGSEAVLSVSRL----GERRG 661
 Qy 715 KDP-----KPEAILTPLMHNGKLATPGNTAKMLIKADQHHLDTALPTPESTP 762
 Db 662 TGPGRGGAGGGPGGPPEALLAPLMQNGW-----TKAALLHGGPHDLDTGLLPTEQTP 715
 Qy 763 TLQQKRKP-----SRGSREWERNQNLINACTKDMPPMGSPVIPTDL----PLRASPSH 811
 Db 716 -LPQKRLPTPHPHAHALGSRWDHSHALLSASAS-----TSLLLLAPARASEQ- 762
 Qy 812 IPSVVVLPIITQQGYQHEYVDQP---KMSEVAQMALEDQAATLEYKTIKEHLSSKSPNHGV 868
 Db 763 -PQVPAEPGPE-----SRLCAPRSCRASHPGDFPLTPHASPDORRRVVSAPTGPLDPSVG- 815
 Qy 869 NLVENLDLSP-PKVPQREASL-----GPPGASLSQTGLSKRLEMHHSSSYGVYKRSYP 921
 Db 816 -----DGLPGPWSPATSSLRRPGPHGPPTAALRRT-----HTFNSG----EARP 856
 Qy 922 TNSLTRSHQATTLKRNTNSSNSSHLNRNQSFGRGD-NPPAP 963
 Db 857 GGHRPRRHP-----PADSTHL---LPCGTGERTAPPVP 886

RESULT 6

SM6C_HUMAN

ID SM6C_HUMAN STANDARD; PRT; 930 AA.
 AC Q9H3T2; Q8WXT8; Q8WXT9; Q8WXU0; Q96JF8;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Semaphorin 6C precursor (Semaphorin Y) (Sema Y).
 GN SEMA6C OR SEMAY OR KIAA1869.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Brain;
 RA Kimura T., Ishida H.;
 RL Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
 RC TISSUE=Brain;
 RA Qu X., Zhai Y., Wei H., Zhang C., Xing G., Yu Y., Wu S., Zhang Y.,
 RA Ouyang S., Zhou G., He F.;
 RL Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Brain;
 RX MEDLINE=21245130; PubMed=11347906;

RA Nagase T., Nakayama M., Nakajima D., Kikuno R., Ohara O.;
 RT "Prediction of the coding sequences of unidentified human genes. XX.
 RT The complete sequences of 100 new cDNA clones from brain which code
 RT for large proteins in vitro.";
 RL DNA Res. 8:85-95(2001).
 CC -!- FUNCTION: May be a stop signal for the dorsal root ganglion
 CC neurons in their target areas, and possibly also for other
 CC neurons. May also be involved in the maintenance and remodeling of
 CC neuronal connections (By similarity).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=3;
 CC Name=1; Synonyms=Short 1;
 CC IsoId=Q9H3T2-1; Sequence=Displayed;
 CC Name=2; Synonyms=Short 2;
 CC IsoId=Q9H3T2-2; Sequence=VSP_006046, VSP_006047;
 CC Name=3; Synonyms=Long;
 CC IsoId=Q9H3T2-3; Sequence=VSP_006047;
 CC -!- SIMILARITY: Belongs to the semaphorin family.
 CC -!- SIMILARITY: Contains 1 Sema domain.
 CC -----
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 CC -----
 DR EMBL; AB022434; BAB20670.1; -.
 DR EMBL; AF339152; AAL72098.1; -.
 DR EMBL; AF339153; AAL72099.1; -.
 DR EMBL; AF339154; AAL72100.1; -.
 DR EMBL; AB058772; BAB47498.1; ALT_INIT.
 DR Genew; HGNC:10740; SEMA6C.
 DR InterPro; IPR003659; Plexin-like.
 DR InterPro; IPR001627; Sema.
 DR Pfam; PF01403; Sema; 1.
 DR SMART; SM00423; PSI; 1.
 DR SMART; SM00630; Sema; 1.
 KW Signal; Transmembrane; Multigene family; Neurogenesis; Glycoprotein;
 KW Developmental protein; Alternative splicing.
 FT SIGNAL 1 24 POTENTIAL.
 FT CHAIN 25 930 SEMAPHORIN 6C.
 FT DOMAIN 25 604 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 605 625 POTENTIAL.
 FT DOMAIN 626 930 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 233 540 SEMA.
 FT DOMAIN 662 667 POLY-PRO.
 FT DOMAIN 752 755 POLY-PRO.
 FT CARBOHYD 70 70 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 286 286 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 437 437 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARSPLIC 184 223 Missing (in isoform 2).
 FT /FTId=VSP_006046.
 FT VARSPLIC 586 586 Y -> YVLPGGPGSPGTPSPPSDAHPRPQSSTLGVHTR
 FT (in isoform 2 and isoform 3).

FT /FTId=VSP_006047.
 FT CONFLICT 125 125 I -> V (IN REF. 2; AAL72099).
 FT CONFLICT 252 252 R -> K (IN REF. 1).
 FT CONFLICT 455 455 P -> T (IN REF. 1 AND 3).
 SQ SEQUENCE 930 AA; 99682 MW; 8AF8814ADBC84C88 CRC64;

Query Match 27.8%; Score 1515.5; DB 1; Length 930;
 Best Local Similarity 35.8%; Pred. No. 5.3e-90;
 Matches 380; Conservative 136; Mismatches 356; Indels 189; Gaps 32;

Qy 6 LLLYFTLLHFAGAGFPEDSEPISISHGNYTKQYPVFVGHKPGRNTTQRHRLDIQMIMIMN 65
 ||| :| | | ||:| |: || | | : | | | :| |
 Db 13 LLLLLSLPH-TQAAFPQDPLPLLLISDLQGTSPLSWFRGLEDDAVAAEL-GLDFQRFLLTN 70

Qy 66 GTLYIAARDHIYTVDIDTSHT-EEIYCSKKLTWKSQRQADVDCRMKGKHKDECHNFIKVL 124
 || :||| |::| |: | : | |||:| |: | :|| | |||:|:| |
 Db 71 RTLLVAARDHVFSFDLQAEEEGGLVPNKYLWRSQ--DVENCAVRGKLTDECYNYIRVL 128

Qy 125 LKKNDDALFVCGTNAFNPSCRNYKMDTLEPFGDEFSGMARCPYDAKHANVALFADGKLYS 184
 : : | |||:|:| ||:| : :| :| | | |||:| | :|||:|:| | |
 Db 129 VPWDSQTLACGTNSFSPVCRSYGITSLQQEGEELSGQARCPFDATQSNVAIFAEGSLYS 188

Qy 185 ATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYFFFREIAVEYN 244
 || || | |||:| || | ||: | :|||:|:| |||:|:|:|:|:|:|:|:|
 Db 189 ATAADFQASDAVVYRSLGQPPLRSKAYDSKWLREPHFVQALEHGDHVYFFFREVSVEDA 248

Qy 245 TMGKVVFPFVAQVCKNDMGGSQVRLEKQWTSFLKARLNCSVPGDSHFYFNILQAVTDVIR 304
 :|:| | |||:| | ||| | | :| ||| | ||| | ||| | |||:| | :
 Db 249 RLGRVQFSRVARVCKRDMGGSPRALDRHWTSLKLRLNCSVPGDSTFYFDVLQALTGPVN 308

Qy 305 INGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVDERVPKP 364
 ::|| : | :| ||| | |||:| : :| | | :|||:| | ||| :||| |
 Db 309 LHGRSALFGVFTTQTNSIPGSAVCAFYLDEIERGFEGKFKEQSRSLDGAWTPVSEDRVPSP 368

Qy 365 RPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRLTKIA 424
 ||| ||| :::| : ||| | ||| |||:| ||| : :| | | ||:|
 Db 369 RPGSCAGVGGAALFSSSRDLDPDDVLTFIKAHPLLDPAVPPVTHQP-LLTLTSRALLTQVA 427

Qy 425 VDTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLNDSLFLEEMSVYNSEKCSYDGVED 484
 || |||:| ||:| || | :|| | | || : : |||: | : :||
 Db 428 VDMAGPHSNITVMFLGSNDGTVLKVLPPGGRSGG-PEPILLEEIDAYSPARCSGKRTAQ 486

Qy 485 --KRIMGMLDRASSSLYVAFSTCVIKVPLGRGERHGKCKKTCIASRDPYCGWIKEGGAC 542
 :||:|:| | :||| |::| || || || |::|:|:|:| ||| | |
 Db 487 TARRIIGLELDTEGHRLFVAFSGCIVYLP LSRCARHGACQRSCLASQDPYCGWHSSRG-C 545

Qy 543 SHLSPNSRLTFEQDIERGNTDGL--GDCHNSFVALNGHSSSLLPSTTTSDSTAQEGYESR 600
 : : :| || : : ||| : :| : |
 Db 546 VDIRGSGGTDVDQ---AGNQESMEHGDCQDG-----ATGSQSGPGDSAY--- 586

Qy 601 GGMLDWKHLSDSPDSTDPLGAVSSHNHQQDKKGVIRESYLKGHQDLVPVTLIAIVILAFV 660
 || |: : ||: || :| ||
 Db 587 -----GVERRDLPPASASRSVPIPLLLASVAAFA 615

Qy 661 MGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRG-----SMSSVTKLSGL 708
 :|| ||: | | | | | | | | :| :| :| |
 Db 616 LGASVSGLLVSCAC--RR-----AHRRGKDIETPGLPRPLSLRSLARLHG- 659

Qy 709 FGDTQSKDPKP--EAILTPLMHNGKLIATPGNTAKMLIKADQHHLDTALPTPESTPTLQQ 766
 | : | : | | : : | | : | | | | | | |
 Db 660 -GGPEPPPPSKDGDVQTPQLYTTFPPPEGVPPP-----ELACLPTPESTPELPV 709

Qy 767 KRKPSRGSREWERNQNLINACTKDMPPMGSPVIPTDLPLRASPSH-----IPSVVVLPIIT 821
 | : | | | | | | : | | : | | : | |
 Db 710 KHLRAAGD-PWEWNQNRNNA-----KEGPGRSRGGHAAGGPAPRVLVLP-- 752

Qy 822 QQGYQHEYVDQPKMSEVAQMALEDQAATLEYKTIKEHL----SSKSPNHGVNLVENLDS- 876
 | | | | | : | | : | | : | | | |
 Db 753 -----PPPGCPGQ-----AVEVTTLEELLRYLHGPQPPRKGAEPPAPLTSR 793

Qy 877 -LPPKVPQREASLGPPGASLSQTGLSKRLEMHHSSSYGV DYKRSYPTNSLTRSHQATTLK 935
 | | | : | | | : | | : | | | | |
 Db 794 ALPPE--PAPALLGGPSRPHECASPLRLDV-----PPEGRCASAPA---- 833

Qy 936 RNNTNSSNSSHL----SRNQSFGRGDNPPAPQVRVDSIQVHSSQPSGQAVTVSRQPS--- 988
 | : : | | | | | | | | | | | |
 Db 834 -RPALSAPAPRLGVGGGRRLLPFSGHRAPPALLTRV-----PSGGPSRYSGGPGKHL 883

Qy 989 --LNAYNSLTRSGLKRTPSLKPDPVPPKPSF-APLSTSMKPN 1026
 | | | | | : | | | | | |
 Db 884 LYLGRPEGYRGRALKRV DVEKPLSLKPPLVGPSSRQAVPN 924

RESULT 7

SM6C_MOUSE

ID SM6C_MOUSE STANDARD; PRT; 931 AA.
 AC Q9WTM3;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Semaphorin 6C precursor (Semaphorin Y) (Sema Y).
 GN SEMA6C OR SEMAY.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RX MEDLINE=99160821; PubMed=10049528;
 RA Kikuchi K., Chedotal A., Hanafusa H., Ujimasa Y., de Castro F.,
 RA Goodman C.S., Kimura T.;
 RT "Cloning and characterization of a novel class VI semaphorin,
 RT semaphorin Y.";
 RL Mol. Cell. Neurosci. 13:9-23(1999).
 CC -!- FUNCTION: May be a stop signal for the dorsal root ganglion
 CC neurons in their target areas, and possibly also for other
 CC neurons. May also be involved in the maintenance and remodeling of
 CC neuronal connections (By similarity).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- SIMILARITY: Belongs to the semaphorin family.
 CC -!- SIMILARITY: Contains 1 Sema domain.
 CC -----
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 DR EMBL; AB013729; BAA76294.1; -.
 DR MGD; MGI:1338032; Sema6c.
 DR InterPro; IPR001627; Sema.
 DR Pfam; PF01403; Sema; 1.
 DR SMART; SM00630; Sema; 1.
 KW Signal; Transmembrane; Multigene family; Neurogenesis; Glycoprotein;
 KW Developmental protein.
 FT SIGNAL 1 25 POTENTIAL.
 FT CHAIN 26 931 SEMAPHORIN 6C.
 FT DOMAIN 26 605 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 606 626 POTENTIAL.
 FT DOMAIN 627 931 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 234 541 SEMA.
 FT DOMAIN 663 669 POLY-PRO.
 FT DOMAIN 754 757 POLY-PRO.
 FT CARBOHYD 71 71 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 287 287 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 438 438 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 931 AA; 99537 MW; B0D99D594209F125 CRC64;

Query Match 27.4%; Score 1493.5; DB 1; Length 931;
 Best Local Similarity 35.7%; Pred. No. 1.4e-88;
 Matches 374; Conservative 145; Mismatches 353; Indels 177; Gaps 32;

Qy 6 LLLYFTLLHFAGAGFPEDSEPISSISHGNYTKQYPVFVGHKPGRNTTQRHRLDIQMIMIN 65
 ||| : | | | ||: | : | | : : || | : : |
 Db 13 LLLLLSSLPQAQAAPQDPTPLLTSDIQGASPSWFRGLEDDAVAAEL-GLDFQRFLTLN 71
 Qy 66 GTLYIAARDHIYTVDIDTSHT-EEIYCSKKLTWKSQRQADVDTCRMKGKHKDECHNFIKVL 124
 || : ||||| : : | : : | ||| : | : : | : || | ||| : : ||
 Db 72 RTLLVAARDHVFSFDLQAQEEGGLVLPNKFLTWRSQ--DMENCAVRGKLTDECYNYIRVL 129
 Qy 125 LKKND DALFVCGTNAFNPSCRNYKMDTLEPFGDEFSGMARCPYDAKHANVALFADGKLYS 184
 : | | |||| : | || : : : | : | || ||| : || : ||| : ||
 Db 130 VPWNSQTLLACGTNSFSMPCRSYGITSLQQEGEELSGQARCPFDATQSTVAIFAEGSLYS 189
 Qy 185 ATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDYIYFFFREIAVEYN 244
 || || | ||| : |||| | || : ||||| : ||| || : || : ||||| : ||
 Db 190 ATAADFQASDAVVYRSLGPQPLRSKYDSKWLREPHFVYALEHGEHVYFFFREVSVEDA 249
 Qy 245 TMGKVVFPRAQVCKNDMGGSQRVLEKQWTSFLKARLNCVPGDSHFYFNILQAVTDVIR 304
 : : | | ||| : || |||| | : : ||||| ||||| ||||| ||| : ||| :
 Db 250 RLGRVQFSRVARVCKRDMGGSPRALDRHWTSFLKLRLNCVPGDSTFYFDVLQSLTGPN 309
 Qy 305 INGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVDERVPKP 364
 : : || : | : | ||||| ||| : || | : |||| : | |||| : : || |
 Db 310 LHGRSALFGVFTTQTNSIPGSAVCAFYLLDDIERGFEGKFKEQSRSLDGAWTPVSEDKVPSP 369
 Qy 365 RPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRLTKIA 424
 ||| ||| : : : | : || | || | ||| : || : | | ||| :

Db 370 RPGSCAGVGAAASFSSSQDLPPDDVLLFIKAHPLLDPAVPPATHQP-LLTLTSRALLTQVA 428

Qy 425 VDTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLNDSLFLEEMSVYNSEKCSYDGVED 484
 || |||::| ||:|||| | :|| | | :: : |||: |: :|| |

Db 429 VDMAGPHRNTTVLFLGSNDGTVLKVLPP-GGQSLGSEPIVLEEIDAYSHARCS--GKRS 485

Qy 485 ----KRIMGMLDRASSSLYVAFSTCVIKVPLGRGERHGKCKKTCIASRDPYCGWIKEGG 540
 :||:|::|| |:||| |:: : | || ||| |::|:|| ||||| : |

Db 486 PRAARRIIGLELDTTEGHRLFVAFPGCIVYLSLSRCARHGACQRSCLASLDPYCGWHRSRG 545

Qy 541 ACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALNGHSSSLLPSTTTSDSTAQEGYE-S 599
 | | | || | | | : | | | : | | | : | | |

Db 546 CMSIRGP-----GGTD-----VDLTGNQES-----TEHGDCQDGATGS 578

Qy 600 RGGMLDWKHLLDSPDSTDPLGAVSSHNHQDKKGVIRESYLKGHDLVPTLLAIAVILAF 659
 : | | : | | | | | | | | | | | | | | | | | |

Db 579 QSGPGDSAY-----GVRDLSPASASRSIPIPLLLACVAAAF 615

Qy 660 VMGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRGSMSSVTKLSGLFGDTQSKDKPKP 719
 :|| ||: | | | || : :||: ||: | : | | | | |

Db 616 ALGASVSGLLVSCAC--RRAN----RRRSKDIETPGLPRPLSLRSLARLHGCGPEPPPPP 669

Qy 720 ---EAILTPLMHNGKLATPGNTAKMLIKADQHHLDTALPTPESTPTLQQKRKPSRGSRE 776
 :| || :: | | : :| ||||:| | | : |

Db 670 KDGDAAQTPQLYTTFLPPPDGGSPP-----ELACLPTPETTPELPVKHLRASGG-P 719

Qy 777 WERNQNLINACT-KDMPPMGSPVIPTDLP---LRASPHIPSVVVLPTQQ---GYQH-- 827
 || ||| || || | | | :| | | | | | : | | |

Db 720 WEWNQNGNNASEGPRPPRGCSGAGGPAPRVLRPPPGCPGQAVEVTTLEELLRYLHGP 779

Qy 828 -----EYVDQPKMSEVAQMALEDQAATLEYKTIKEHLSSKSPNHGVNLVENL 874
 : :| || | | | | | | | | | | | | | |

Db 780 QPPRGKSEPLASAPFTSRPPASEPGASLFVD-----SSPMRDPVPPL-RL 824

Qy 875 DSLPPK----VPQREASLGPPGASLSQTGLSKRLEMHHSSSYGVDYKRSYPTNSLTRSHQ 930
 | :||: | :| | | | | :|| | :

Db 825 D-VPPEGKRAAPSGRPALSAPAPRLG-VGGSRL-----PFPT-----HR 862

Qy 931 ATTLKRNTNTSSNSSHLNRNQSFGRGDNPPAPQRVDS--IQVHSSQPSGQAVTVSRQPS 988
 | | | | | | | | :| | : : | |

Db 863 A-----PPGLLTRVPSGGPARYSGGPGRHLLYLGR-PE 894

Qy 989 LNAYNSLTRSGLKRTPSLKPDV--PPKPS 1015
 : || | :| | || : ||:|:

Db 895 GHRGRSLKRVDVKSPSPKPLASPPQPA 923

RESULT 8

SM6C_RAT

ID SM6C_RAT STANDARD; PRT; 960 AA.

AC Q9WTL3; Q9WTM6;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Semaphorin 6C precursor (Semaphorin Y) (Sema Y).

GN SEMA6C OR SEMAY.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS SEMA Y-L AND SEMA Y-S).
 RC STRAIN=Sprague-Dawley; TISSUE=Muscle;
 RX MEDLINE=99160821; PubMed=10049528;
 RA Kikuchi K., Chedotal A., Hanafusa H., Ujimasa Y., de Castro F.,
 RA Goodman C.S., Kimura T.;
 RT "Cloning and characterization of a novel class VI semaphorin,
 RT semaphorin Y.";
 RL Mol. Cell. Neurosci. 13:9-23(1999).
 CC -!- FUNCTION: SHOWS GROWTH CONE COLLAPSING ACTIVITY ON DORSAL ROOT
 CC GANGLION (DRG) NEURONS IN VITRO. MAY BE A STOP SIGNAL FOR THE DRG
 CC NEURONS IN THEIR TARGET AREAS, AND POSSIBLY ALSO FOR OTHER
 CC NEURONS. MAY ALSO BE INVOLVED IN THE MAINTENANCE AND REMODELING OF
 CC NEURONAL CONNECTIONS.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=Sema Y-L;
 CC IsoId=Q9WTL3-1; Sequence=Displayed;
 CC Name=Sema Y-S;
 CC IsoId=Q9WTL3-2; Sequence=VSP_006048;
 CC -!- TISSUE SPECIFICITY: Expressed in many regions of the developing
 CC nervous system, probably in neurons and their precursors, but also
 CC in nonneural tissue such as immature muscle and dermis. In adult,
 CC strong expression in the skeletal muscle and moderate expression
 CC in the brain, where cerebellum shows the highest expression. Also
 CC expressed in almost all areas of the CNS.
 CC -!- DEVELOPMENTAL STAGE: DETECTED AT E12 AND FOUND AT MARKEDLY
 CC INCREASED LEVELS AT E15 AND E18 IN BOTH THE HEAD AND THE BODY. AT
 CC BIRTH THE LEVEL DECREASES SIGNIFICANTLY.
 CC -!- SIMILARITY: Belongs to the semaphorin family.
 CC -!- SIMILARITY: Contains 1 Sema domain.
 CC -----
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 CC -----
 DR EMBL; AB000817; BAA76293.2; -.
 DR EMBL; AB014074; BAA76295.1; -.
 DR InterPro; IPR001627; Sema.
 DR Pfam; PF01403; Sema; 1.
 DR SMART; SM00630; Sema; 1.
 KW Signal; Transmembrane; Multigene family; Neurogenesis; Glycoprotein;
 KW Developmental protein; Alternative splicing.
 FT SIGNAL 1 23 POTENTIAL.
 FT CHAIN 24 960 SEMAPHORIN 6C.
 FT DOMAIN 24 635 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 636 656 POTENTIAL.
 FT DOMAIN 657 960 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 234 541 SEMA.

Qy 649 TLLAIAVILAFVMGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRRGSMSSVTKL SGL 708
 || | || :|| ||: | | | || : :|: |:| | : | : |
 Db 635 PLLLACVAAAFALGASVSGLLVSCAC--RRAN----RRRSKDIETPGLPRPLSLRSLARL 688

Qy 709 FGDTQSKDPKP---EAILTPLMHNGKLATPGNTAKMLIKADQHHLDTALPTPESTPTLQ 765
 | | | :| || :| | | : :| ||||:| | |
 Db 689 HGGGPEPPPPPKDGDAAQTPQLYTTFLPPPEGGSPP-----ELACLPTPETTPELP 739

Qy 766 QKRKPSRGSREWERNQNLINACTKDMPPMGSPVIPTDLP---LRASPSHIPSVVLPITQ 822
 | : | || || | | | | :| | | | | |
 Db 740 VKHLRASGG-PWEWNQNGNNASEGPRPRGCSAAGGPAPRVLVRPPPGCPGQEEVEVTTL 798

Qy 823 Q---GYQH-----EYVDQPKMSEVAQMALEDQAATLEYKTIKEHLSSKSP 864
 : | | : :| || | | || |
 Db 799 EELLRYLHGPPQPPRKGEPLASAPFTSRPPASEPGAALFVD-----SSPMP 844

Qy 865 NHGVNLVENLDSLPP-----KVPQREASLGPPGASLSQTGLSKRLEMHHSSSYG 913
 | :|| | :| | | :| | :||
 Db 845 R-----DCVPPLRLDVPDPDGKRAAPSGRPALSAPAPRLGVSG-SRRL----- 885

Qy 914 VDYKRSYPTNSLTRSHQATTLKRNTNSSNSSHL SRNQSFGRGDNPPAPQRVDS--IQV 971
 :|| | :| | | || || |
 Db 886 -----PFPT-----HRA-----PPGLLTRVPSGGPSR 907

Qy 972 HSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRTPSLKPDV--PPKPS 1015
 :| | : :| | : || | :| | | : ||:|
 Db 908 YSGGPGRHLLYLGR-PDGHGRSLKRV DVKSPLSPKPPLATPPQPA 952

RESULT 9

SM1A_SCHAM

ID SM1A_SCHAM STANDARD; PRT; 730 AA.

AC Q26473;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Semaphorin 1A precursor (Semaphorin-I) (Sema I) (Fasciclin IV).

GN SEMA-1A OR FAS4.

OS Schistocerca americana (American grasshopper).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;

OC Acridoidea; Acrididae; Cyrtacanthacridinae; Schistocerca.

OX NCBI_TaxID=7009;

RN [1]

RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

RX MEDLINE=93040225; PubMed=1418998;

RA Kolodkin A.L., Matthes D.J., O'Connor T.P., Patel N.H., Admon A.,

RA Bentley D., Goodman C.S.;

RT "Fasciclin IV: sequence, expression, and function during growth cone

RT guidance in the grasshopper embryo.;"

RL Neuron 9:831-845(1992).

CC -!- FUNCTION: PLAY A ROLE IN GROWTH CONES GUIDANCE.

CC -!- SUBCELLULAR LOCATION: Type I membrane protein.

CC -!- TISSUE SPECIFICITY: DYNAMICALLY EXPRESSED ON A SUBSET OF AXON

CC PATHWAYS IN THE DEVELOPING CNS AND ON CIRCUMFERENTIAL BANDS OF

CC EPITHELIAL CELLS IN DEVELOPING LIMB BUDS.

CC -!- SIMILARITY: Belongs to the semaphorin family.

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CC      -!- SIMILARITY: Contains 1 Sema domain.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; L00709; AAA29808.1; -.
DR      PIR; JH0798; JH0798.
DR      InterPro; IPR003659; Plexin-like.
DR      InterPro; IPR002165; Plexin_repeat.
DR      InterPro; IPR001627; Sema.
DR      Pfam; PF01437; PSI; 1.
DR      Pfam; PF01403; Sema; 1.
DR      SMART; SM00423; PSI; 1.
DR      SMART; SM00630; Sema; 1.
KW      Signal; Developmental protein; Transmembrane; Glycoprotein;
KW      Neurogenesis.
FT      SIGNAL          1      20      POTENTIAL.
FT      CHAIN           21     730     SEMAPHORIN 1A.
FT      DOMAIN          21     630     EXTRACELLULAR (POTENTIAL).
FT      TRANSMEM        631     651     POTENTIAL.
FT      DOMAIN          652     730     CYTOPLASMIC (POTENTIAL).
FT      DOMAIN          215     515     SEMA.
FT      DOMAIN          217     222     POLY-PHE.
FT      CARBOHYD         44      44     N-LINKED (GLCNAC. . .) (POTENTIAL).
FT      CARBOHYD         71      71     N-LINKED (GLCNAC. . .) (POTENTIAL).
FT      CARBOHYD        163     163     N-LINKED (GLCNAC. . .) (POTENTIAL).
FT      CARBOHYD        267     267     N-LINKED (GLCNAC. . .) (POTENTIAL).
FT      CARBOHYD        360     360     N-LINKED (GLCNAC. . .) (POTENTIAL).
FT      CARBOHYD        539     539     N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ      SEQUENCE       730 AA;  81214 MW;  6D625946E7F8E57F CRC64;

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Query Match          17.8%; Score 971.5; DB 1; Length 730;
Best Local Similarity 34.4%; Pred. No. 4.8e-55;
Matches 244; Conservative 124; Mismatches 224; Indels 117; Gaps 29;

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Qy      8 LYFTLLHFAGAGFPEDSEPISISHGNYTKQYPVFVGHKPGRNTTQR-----HRLDIQMI 61
      | : || | : | | | | | | | | | | | | | | | | : ::
Db      11 LLWVALH--AAAWVNDVSP-----KMYVQF-----GEERVQRFGLGNESHKDHFKLL 54

Qy      62 MIMNGTLYIAARDHIYTVDID--TSHTEEIYCSKKLTWKSQRQADVDTCRMKGKHKDECHN 119
      : : | : || : | : : | || : : : | | | : | : || : | : |
Db      55 EKDHNSLLVGARNIVYNISLRDLTEFTEQ-----RIEWHSSGAHRELCYLKGKSEDDCQN 109

Qy      120 FIKVLLKKND DALFVCGTNAFNPSCRNYKMDTLEPFGD-----EFSGMARCPYDAKHANV 174
      : | : || | : || : : || || : | || : | | : | | : | :
Db      110 YIRVLAKIDDDRVLICGTNAYKPLCRHYALKD----GDYVVEKEYEGRGLCPFPDPHNST 165

Qy      175 ALFADGKLYSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYF 234
      | : : : | : || || | | : || | || : | | | | || : : | : | : |
Db      166 AIYSEGQLYSATVADFSGTDPLIYRG-----PLRTERS DLKQLNAPNFVNTMEYNDFFIFF 220

Qy      235 FFREIAVEYNTMGKVVFPRVAQVCKNDMGGSQRVLEKQWTSFLKARLNCVPGD SHFYFN 294

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Db	221	FFRETAVEYINCGKAIYSRVARVCKHDKGGPHQFGDR-WTSFLKSRLNCSVPGDYPFYFN	279
QY	295	ILQAVTDVIRIN-GRDV---VLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPD	350
Db	280	EQSTSDIIEGNYGGQVEKLIYGVFTTPVNSIGGSAVCAFSMKSILESFDGPFKEQETMN	339
QY	351	STWTPVPDERVPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPW	410
Db	340	SNWLAVPSLKVPEPRPGQCVND-----SRTLDPDVSVNFVKSHITLMDEAVPAFFTRPI	391
QY	411	FLRTMVRYRLTKIAVD----TAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLN-----	461
Db	392	LIRISLQYRFTKIAVDQQVPTPDG--KAYDVLFIGTDDGKVIKAL----NSASFDSSDTV	445
QY	462	DSLFEEMSVYNSEKCSYDGVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRC--ERHG	519
Db	446	DSVVIEELQVLP-----PGVPVKNLVVRMDGDDSKLVVSDDEILAIKLHRCGSDKIT	499
QY	520	KCKKTCIASRDPYCGWIKEGGACSHL-SPN---SRLTFEQDIERGNTDGLGDCHNSFVAL	575
Db	500	NCRE-CVSLQDPYCAWDNVELKCTAVGSPDWSAGKRRFIQNISLGEHKACGGRPQTEIV-	557
QY	576	NGHSSSLLPSTTTSDSTA-----QEGYESRGGMLDWKHLSDPDSTDPLGAVSSHNHQ	628
Db	558	----ASPVPTQPTTKSSGDPVHSIHQAEFEPE---IDNEIVIGVDDSNVIPNTLAEINHA	610
QY	629	DKKGVIRESYLKGHDLQVLPV----TL-LAI-----AVILAFVMGAVFS	666
Db	611	GSK-----LPSSQEKLPITYAETLTIAIVTSCLGALVVGFI SGFLFS	652

RESULT 10

SM1A_DROME

ID SM1A_DROME STANDARD; PRT; 771 AA.

AC Q24322;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Semaphorin 1A precursor (Semaphorin-I) (Sema I).

GN SEMA-1A OR DSEMA-I OR CG18405.

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

OX NCBI_TaxID=7227;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Embryo;

RX MEDLINE=94094332; PubMed=8269517;

RA Kolodkin A.L., Matthes D.J., Goodman C.S.;

RT "The semaphorin genes encode a family of transmembrane and secreted

RT growth cone guidance molecules.";

RL Cell 75:1389-1399(1993).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=Berkeley;

RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
 RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 CC -!- FUNCTION: PLAY A ROLE IN GROWTH CONES GUIDANCE.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- TISSUE SPECIFICITY: EXPRESSED BY SUBSETS OF NEURONS AND MUSCLES.
 CC -!- DEVELOPMENTAL STAGE: EXPRESSION BEGINS AROUND STAGE 10, PRIMARILY
 CC IN THE DEVELOPING CNS. IN STAGE 16 EMBRYOS, IT IS EXPRESSED AT
 CC HIGHEST LEVELS THROUGHOUT THE CNS, AND WEAK EXPRESSION IS SEEN IN
 CC PORTIONS OF THE PERIPHERAL NERVOUS SYSTEM, MOST CLEARLY IN THE
 CC LATERAL SENSORY CLUSTERS.
 CC -!- SIMILARITY: Belongs to the semaphorin family.
 CC -!- SIMILARITY: Contains 1 Sema domain.
 CC -----
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CC -----
 DR EMBL; L26082; AAA88789.1; -.
 DR EMBL; AE003621; AAF52696.1; -.
 DR FlyBase; FBgn0011259; Sema-1a.
 DR InterPro; IPR003659; Plexin-like.
 DR InterPro; IPR002165; Plexin_repeat.
 DR InterPro; IPR001627; Sema.
 DR Pfam; PF01437; PSI; 1.
 DR Pfam; PF01403; Sema; 1.
 DR SMART; SM00423; PSI; 1.
 DR SMART; SM00630; Sema; 1.
 KW Signal; Developmental protein; Transmembrane; Glycoprotein;
 KW Neurogenesis.
 FT SIGNAL 1 19 POTENTIAL.
 FT CHAIN 20 771 SEMAPHORIN 1A.
 FT DOMAIN 21 608 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 609 629 POTENTIAL.
 FT DOMAIN 630 771 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 210 519 SEMA.
 FT DOMAIN 689 694 POLY-PRO.
 FT CARBOHYD 41 41 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 68 68 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 138 138 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 158 158 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 355 355 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 771 AA; 86935 MW; 752E7DD516F32DA5 CRC64;

Query Match 17.1%; Score 932.5; DB 1; Length 771;
 Best Local Similarity 35.0%; Pred. No. 1.7e-52;
 Matches 219; Conservative 106; Mismatches 213; Indels 87; Gaps 20;

Qy 67 TLYIAARDHIYTVDIDTSHTEEIYCSKKLTWKSQADVDTCRMKGKHKDECHNFIKVLK 126
 :| | ||: :: : | :: :| | | : | | :|| :: | |:|:::
 Db 57 SLLIGARNTVFNLISI-----HDLVEQQLRVLTSPEDDTKMCLVKGKDEEACQNYIRIMVV 111
 Qy 127 KNDDALFVCGTNAFNPSCRNYKMD----TLEPFGDEFSGMARCPYDAKHANVALFADGKL 182
 : | | | | | | :| | | : | | | | :| | | | :| : :: | | :|
 Db 112 PSPGRLFVCGTNSFRPMCNTYIISDSNYTLEA---TKNGQAVCPYDPRHNSTSVLADNEL 168
 Qy 183 YSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYFFFREIAVE 242
 || || || | :|| | :| :|| | | | : ||: |||| ||
 Db 169 YSGTVADFGSDPIIYRE-----PLQTEQYDSLNLNAPNFVSSFTQGDFVYFFFRETAVE 223
 Qy 243 YNTMGKVVFPRVAQVCKNDMGGSQRVLEKQWTSFLKARLNCVPGDSHFYFNILQAVTDV 302
 : || :: ||: || | || | : ||||: ||||: || || | :| : ::
 Db 224 FINCGKAIYSRVARVCKWDKGGPHR-FRNRWTSFLKSRLNCSIPGDYPFYFNEIQSASNL 282
 Qy 303 IR----INGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVPD 358
 : :: |: || |||| ||||: : || | | : || | :
 Db 283 VEGQYGSMSSKLIYGVENTPSNSIPGSAVCAFALQDIADTFEGQFKEQTGINSNWLVPVN 342
 Qy 359 ERVPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRY 418
 :|| |||| | : | || |||| || || ||: |:| :|| |
 Db 343 AKVPDPRPGSC-----HNSRALPDPTLNFIKTHSLMDENVPAFFSQPILVRTSTIY 394
 Qy 419 RLTKIAVD-----TAAGPYQNHTVVFLGSEKGIILKFL-ARIGNSGFLNDSLFLLEMSVYN 473

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      | :| | | |   | | : : | :| :| :| | :|   | : :| | : |
Db      395 RFTQIAVDAQIKTPGG--KTYDVIFVGTDLHGKIIKSVNAESADSADKVTSVVIEEIDVLT 452

QY      474 SEKCSYDGVEDKRIM-GMQLDRASSSLY-----VAFSTCVIKVPLGRC--ERHGKCKKT 524
      : : : | : | | | :   |   :   : | : : | | | : :   | :
Db      453 KS-----EPIRNLEIVRTMQYDQPKDGSYDDGKLIIVTDSQVVAIQLHRCHNDKITSCSE- 507

QY      525 CIASRDYPYCGWIKEGGAC-SHLSPN--SRLTFEQDIERGNTDGLGDCHNSFVALNGHSSS 581
      | : | :| | | | | | | | | | :|   | | : : |   | : :
Db      508 CVALQDPYCAWDKIAGKCRSHGAPRWLEENYFYQNVATGQ-----HAAC 551

QY      582 LLPSTTTSDSTAQEGYESRGGMLDWKHLLDSPDSTDPLGAVSSHNHQDKKGVIRESYLKG 641
      : | : | | | | | | | | | | | | | | | | : : |
Db      552 PSGKINSKDANAGEQKGFNRDM----DLLDS-----RRQSKDQEIIDNIDKN 594

QY      642 HDQLVPVTLIAIAVILAFVMGAVFS 666
      : : :   : : | : | :| |
Db      595 FEDIINAQYTVETLVMMAVLGSIIFS 619

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RESULT 11

SM3A_RAT

```

ID      SM3A_RAT          STANDARD;          PRT;    772 AA.
AC      Q63548;
DT      30-MAY-2000 (Rel. 39, Created)
DT      30-MAY-2000 (Rel. 39, Last sequence update)
DT      10-OCT-2003 (Rel. 42, Last annotation update)
DE      Semaphorin 3A precursor (Semaphorin III) (Sema III).
GN      SEMA3A.
OS      Rattus norvegicus (Rat).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX      NCBI_TaxID=10116;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=Wistar; TISSUE=Brain;
RX      MEDLINE=97073089; PubMed=8915837;
RA      Giger R.J., Wolfer D.P., De Wit G.M.J., Verhaagen J.;
RT      "Anatomy of rat semaphorin III/collapsin-1 mRNA expression and
RT      relationship to developing nerve tracts during neuroembryogenesis.";
RL      J. Comp. Neurol. 375:378-392(1996).
CC      -!- FUNCTION: MAY BE INVOLVED IN GUIDING GROWING AXONS TOWARDS THEIR
CC      TARGETS BY FORMING A MOLECULAR BOUNDARY THAT INSTRUCTS AXONS TO
CC      ENGAGE IN THE FORMATION OF SPECIFIC NERVE TRACTS. BINDS TO
CC      NEUROPILIN.
CC      -!- SUBCELLULAR LOCATION: Secreted (By similarity).
CC      -!- DEVELOPMENTAL STAGE: AT E-11, EXPRESSION WAS RESTRICTED TO THE
CC      OLFATORY PIT, THE BASAL AND ROSTRAL SURFACE OF THE TELENCEPHALIC
CC      VESICLE, THE EYE ANLAGE, THE EPITHELIUM OF RATHKE'S POUCH, AND
CC      SOMITES. AT LATER DEVELOPMENTAL STAGES, IT WAS WIDELY DISTRIBUTED
CC      IN NEURONAL AS WELL AS IN MESENCHYMAL AND EPITHELIAL STRUCTURES
CC      OUTSIDE THE NERVOUS SYSTEM. AFTER BIRTH, MESENCHYMAL LEVELS
CC      DECREASED RAPIDLY AND EXPRESSION BECAME RESTRICTED TO SPECIFIC
CC      SETS OF NEURONS IN THE CNS. IN THE MATURE CNS, IT IS DETECTABLE IN
CC      MITRAL CELLS, NEURONS OF THE ACCESSORY BULB AND CEREBRAL CORTEX,
CC      CEREBELLAR PURKINJE CELLS, AS WELL AS A SUBSET OF CRANIAL AND
CC      SPINAL MOTONEURONS.

```

CC -!- DOMAIN: Strong binding to neuropilin is mediated by the carboxy
 CC third of the protein.
 CC -!- SIMILARITY: Belongs to the semaphorin family.
 CC -!- SIMILARITY: Contains 1 Sema domain.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
 CC -----
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 CC -----
 DR EMBL; X95286; CAA64607.1; -.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR003659; Plexin-like.
 DR InterPro; IPR001627; Sema.
 DR Pfam; PF00047; ig; 1.
 DR Pfam; PF01403; Sema; 1.
 DR SMART; SM00409; IG; 1.
 DR SMART; SM00423; PSI; 1.
 DR SMART; SM00630; Sema; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW Signal; Immunoglobulin domain; Multigene family; Neurogenesis;
 KW Developmental protein; Glycoprotein.
 FT SIGNAL 1 20 POTENTIAL.
 FT CHAIN 21 772 SEMAPHORIN 3A.
 FT DOMAIN 240 538 SEMA.
 FT DOMAIN 577 665 IG-LIKE C2-TYPE.
 FT DOMAIN 728 770 ARG/LYS-RICH (BASIC).
 FT DISULFID 650 723 BY SIMILARITY.
 FT CARBOHYD 53 53 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 125 125 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 591 591 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 772 AA; 88808 MW; 240907812FF9F2D2 CRC64;

Query Match 15.7%; Score 858; DB 1; Length 772;
 Best Local Similarity 32.3%; Pred. No. 1.le-47;
 Matches 209; Conservative 104; Mismatches 251; Indels 84; Gaps 20;

Qy 47 GRNTTQRHRLDIQMIMMNGT-----LYIAARDHIYTVDIDT 83
 |:| |:| ::: | ||: |:|::: ::
 Db 25 GKNNVPRKLKLSYKEMLESNNVITFENGLANSSSYHTFLLDEERSRLYVGAKDHIFSFL-- 82
 Qy 84 SHTEEIYCSKKLTWKSQRQADVDTCRMKGKH-KDECHNFIKVLKKNDDALFVCGTNAFNP 142
 | :|: | | : | | | | | | | : | | | | :|
 Db 83 ---VNIKDFQKIVWPVSYTRRDECKWAGKDILKECANFIKVLKAYNQTHLYACGTGAFHP 139
 Qy 143 SCR-----NYKMDTLEPFGDEF--SGMARCPYDAKHANVALFADGKLYSATVTDFLAIDA 195
 | : : | : | : | | | : | | : | | | : |
 Db 140 ICTYIEVGHHPEDNIFKLQDSHFENGRGKSPYDPKLLTASLLIDGELYSGTAAEDFMGRDF 199
 Qy 196 VIYRSLGESPTLRTVKHDSKWLKEPYFVQA-----VDYGDYIYFFFREIAVEYNTMGK 248
 |:|:| | :| :|:|:| :| | : | :| | | | :| :|
 Db 200 AIFRTLGHHPHPIRTEQHDNRWLNDRPFISAHLPESDNPEDDKVYFFFRENAIDGEHSGK 259

RT "Disruption of semaphorin III/D gene causes severe abnormality in
 RT peripheral nerve projection.";
 RL Neuron 19:519-530(1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Kimura T., Fishman M.C.;
 RT "cDNA sequence of mouse collapsin/semaphorin III.";
 RL Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [5]
 RP SEQUENCE OF 107-772 FROM N.A.
 RC TISSUE=Fetal brain;
 RX MEDLINE=95267432; PubMed=7748562;
 RA Messersmith E.K., Leonardo E.D., Shatz C.J., Tessier-Lavigne M.,
 RA Goodman C.S., Kolodkin A.L.;
 RT "Semaphorin III can function as a selective chemorepellent to pattern
 RT sensory projections in the spinal cord.";
 RL Neuron 14:949-959(1995).
 CC -!- FUNCTION: Play a role in growth cones guidance. May function to
 CC pattern sensory projections by selectively repelling axons that
 CC normally terminate dorsally.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- DEVELOPMENTAL STAGE: EXPRESSED EARLY IN EMBRYONIC DEVELOPMENT
 CC (E11) IN DISTINCT REGIONS OF THE NEUROECTODERM AND MESODERM.
 CC EXPRESSION BECAME MORE EXTENSIVE AT LATER STAGES.
 CC -!- DOMAIN: Strong binding to neuropilin is mediated by the carboxy
 CC third of the protein.
 CC -!- SIMILARITY: Belongs to the semaphorin family.
 CC -!- SIMILARITY: Contains 1 Sema domain.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
 CC -----
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CC -----

DR EMBL; X85993; CAA59985.1; -.
 DR EMBL; D85028; BAA19773.1; -.
 DR EMBL; L41541; AAL77611.1; -.
 DR EMBL; BC057588; AAH57588.1; -.
 DR EMBL; L40484; AAA73934.1; -.
 DR PIR; I48747; I48747.
 DR PIR; I58169; I58169.
 DR MGD; MGI:107558; Sema3a.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR003659; Plexin-like.
 DR InterPro; IPR001627; Sema.
 DR Pfam; PF00047; ig; 1.
 DR Pfam; PF01403; Sema; 1.
 DR SMART; SM00409; IG; 1.
 DR SMART; SM00423; PSI; 1.
 DR SMART; SM00630; Sema; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW Signal; Immunoglobulin domain; Multigene family; Neurogenesis;
 KW Developmental protein; Glycoprotein.
 FT SIGNAL 1 20 POTENTIAL.
 FT CHAIN 21 772 SEMAPHORIN 3A.
 FT DOMAIN 240 538 SEMA.
 FT DOMAIN 579 665 IG-LIKE C2-TYPE.
 FT DOMAIN 728 770 ARG/LYS-RICH (BASIC).
 FT DISULFID 650 723 BY SIMILARITY.
 FT CARBOHYD 53 53 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 125 125 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 591 591 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 193 193 D -> N (IN REF. 5).
 FT CONFLICT 207 207 H -> D (IN REF. 1).
 FT CONFLICT 253 253 D -> G (IN REF. 1).
 FT CONFLICT 352 352 F -> L (IN REF. 5).
 FT CONFLICT 403 403 A -> G (IN REF. 1).
 FT CONFLICT 571 572 QH -> ED (IN REF. 1).
 FT CONFLICT 616 620 EDRKE -> RRSKR (IN REF. 1).
 FT CONFLICT 623 623 R -> K (IN REF. 5).
 SQ SEQUENCE 772 AA; 88799 MW; E89A08528B10AEC3 CRC64;

Query Match 15.7%; Score 853; DB 1; Length 772;
 Best Local Similarity 32.2%; Pred. No. 2.3e-47;
 Matches 208; Conservative 102; Mismatches 257; Indels 78; Gaps 18;

Qy 47 GRNTTQRHRLDIQMIMIMNGT-----LYIAARDHIYTVDDIDT 83
 |:| |:| : :: | ||: |:|:: ::
 Db 25 GKNNVPRCLKLSYKEMLESNNVITFNGLANSSSYHTFLLDEERSRLYVGAKDHIFSENL-- 82
 Qy 84 SHTEEIYCSKKLTWKSQRQADVDCRMKGKH-KDECHNFIKVLLKKNDDALFVCGTNAFNP 142
 | :|: | | : | || ||||| | | : ||| ||:|
 Db 83 ---VNIKDFQKIVWPVSYTRRDECKWAGKDILKECANFIKVLEAYNQTHLYACGTGAFHP 139
 Qy 143 SCR-----NYKMDTLEPGFDEF--SGMARCPYDAKHANVALFADGKLYSATVTDFLAIDA 195

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      |      :: | : |      :| : || |      :| ||: || | ||: |
Db      140 ICTYIEVGHHPEDNIFKLQDSHFENGRGKSPYDPKLLTASLLIDGELYSGTAADFMGRDF 199

Qy      196 VIYRSLGESPTLRTVKHDSKWLKEPYFVQA-----VDYGDYIYFFFREIAVEYNTMGK 248
      |:|:| |      :| | :||:| | :| | : |      | :||| | | :| : | |
Db      200 AIFRTLGHHPIRTEQHDNRWLNDRFISAHLPESDNPEDDKVYFFFRENAIDGEHSGK 259

Qy      249 VVFPRVAQVCKNDMGGSQRVLEKQWTSFLKARLNCVPG-----DSHFYFNILQAVTDVIR 304
      |: | :|| | | | | | :| :|:| | | | | | | | | | | | | :| |
Db      260 ATHARIGQICKNDFGG-HRSLVNKWTTFKARLICSVPGPNGIDTHF-----DELQDVFL 313

Qy      305 INGRD----VVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVDER 360
      :| :|      :| | :| | | | | | | | | : | : | : | : | |
Db      314 MNSKDPKNPIVYGVFTTSSNIFKGSAVCMYSMSDVRRVFLGPYAHRDGPYQWVPY-QGR 372

Qy      361 VPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRL 420
      || ||| | | : | : : : || | : | :| | | | | | | | | :| | | :
Db      373 VPYPRPGTCP-SKTFGGFDSTKDLRDDVITFARSHPAMYNPVFPINNRPIMIKTDVNYQF 431

Qy      421 TKIAVDTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLNDSLFLEEMSVYNSEKCSYD 480
      |:| | |      : | :| :| : | :| | : :      : : : | | | :| :
Db      432 TQIVVDRVDAEDGQYDVMFIGTDVGTVLKVVSVPKETWHDLEEVLEEMTVFR----- 484

Qy      481 GVEDKRIMGMLDRASSSLYVAFSTCVIKVPLGRCERHGKCKKTCIASRDPYCGWKEGG 540
      | | | :| | | : | :| | | :| | | | | | | :| | | | | :|
Db      485 --EPTTISAMELSTKQQQLYIGSTAGVAQLPLHRCDIYGKACAECCLARDPYCAW--DGS 540

Qy      541 ACSHLSPNS-RLTFEQDIERGNTDGLGDCHNSFVALNGHSSSL-----LPSTTTSDSTAQE 595
      :| | | : | | | | | | | : | | | | | : | : | : | :
Db      541 SCSRYFPTAKRRTRRRQDIRNG--DPLTHCSDLQHHDNHHGPSLEERIITYGVENSSTFLEC 598

Qy      596 GYESRGGMLDWKHLDDSPDSTDPLGAVSSSHNHQDKKGVIRESYLK 640
      :| : : | : | : : : | : :| :| : | |
Db      599 SPKSQRALVYWQFQRRNEDRKEEI-RMGDHIIRTEQGLLLRSLQK 642

```

RESULT 13

SM3A_HUMAN

ID SM3A_HUMAN STANDARD; PRT; 771 AA.

AC Q14563;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Semaphorin 3A precursor (Semaphorin III) (Sema III).

GN SEMA3A.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Fetal brain;

RX MEDLINE=94094332; PubMed=8269517;

RA Kolodkin A.L., Matthes D.J., Goodman C.S.;

RT "The semaphorin genes encode a family of transmembrane and secreted

RT growth cone guidance molecules.";

RL Cell 75:1389-1399(1993).

RN [2]
 RP SEQUENCE OF 1-37 FROM N.A.
 RA Woessner J., Minx P., Hinds K., Strowmatt C.;
 RL Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
 RN [3]
 RP SEQUENCE OF 39-182 FROM N.A.
 RA Rohlfing T., Tin-Wollam A.M., Duckels G.;
 RL Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
 CC -!- FUNCTION: INDUCES THE COLLAPSE AND PARALYSIS OF NEURONAL GROWTH
 CC CONES. COULD SERVE AS A LIGAND THAT GUIDES SPECIFIC GROWTH CONES
 CC BY A MOTILITY-INHIBITING MECHANISM. BINDS TO THE COMPLEX
 CC NEUROPILIN-1/PLEXIN-1 (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).
 CC -!- DOMAIN: Strong binding to neuropilin is mediated by the carboxy
 CC third of the protein.
 CC -!- SIMILARITY: Belongs to the semaphorin family.
 CC -!- SIMILARITY: Contains 1 Sema domain.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
 CC -----
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 CC -----
 DR EMBL; L26081; AAA65938.1; -.
 DR EMBL; AC004451; -; NOT_ANNOTATED_CDS.
 DR EMBL; AC004848; AAC78622.1; -.
 DR PIR; D49423; D49423.
 DR Genew; HGNC:10723; SEMA3A.
 DR MIM; 603961; -.
 DR GO; GO:0005576; C:extracellular; TAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR003659; Plexin-like.
 DR InterPro; IPR001627; Sema.
 DR Pfam; PF00047; ig; 1.
 DR Pfam; PF01403; Sema; 1.
 DR SMART; SM00409; IG; 1.
 DR SMART; SM00423; PSI; 1.
 DR SMART; SM00630; Sema; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW Signal; Immunoglobulin domain; Multigene family; Neurogenesis;
 KW Developmental protein; Glycoprotein.
 FT SIGNAL 1 20 POTENTIAL.
 FT CHAIN 21 771 SEMAPHORIN 3A.
 FT DOMAIN 240 538 SEMA.
 FT DOMAIN 580 664 IG-LIKE C2-TYPE.
 FT DOMAIN 727 769 ARG/LYS-RICH (BASIC).
 FT DISULFID 649 722 BY SIMILARITY.
 FT CARBOHYD 53 53 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 125 125 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 590 590 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 771 AA; 88889 MW; 9985F8D3EAED8456 CRC64;

Query Match 15.6%; Score 852.5; DB 1; Length 771;
 Best Local Similarity 32.1%; Pred. No. 2.5e-47;
 Matches 208; Conservative 106; Mismatches 250; Indels 83; Gaps 20;

```

Qy      44 HKPGRNTTQRHRLDIQMIMIMNGT-----LYIAARDHIYTVD 80
      :: |:| | :| : :: | ||: |:|:|:| :: |
Db      22 YQNGKNNVPRLKLSYKEMLESNNVITFENGLANSSSYHTFLLDEERSRLYVGAKDHIFSFD 81

Qy      81 IDTSHTEEIYCSKKLTWKSQADVDTCRMKGKH-KDECHNFIKVLLKKND DALFVCGTNA 139
      : | :|: | | :| || || ||||| | |: ||| |
Db      82 L-----VNIKDFQKIVVPVSYTRDECKWAGKDILKECANFIKVLKAYNQTHLYACGTGA 136

Qy     140 FNPSCR-----NYKMDTLEPFGDEF--SGMARCPYDAKHANVALFADGKLYSATVTDFLA 192
      |:| | :|: | : :| : ||| | :| ||:| | | |:
Db     137 FHPICTYIEIGHHPEDNIFKLENSHFENGGRGKSPYDPKLLTASLLIDGELYSGTAADF MG 196

Qy     193 IDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQA-----VDYGDYIYFFFREIAVEYNT 245
      | |:|:| | :|| :|||:| | :| | : | | :| ||||| |::
Db     197 RDFAIFRTLGHHPHPIRTEQHDRWLNDPKFISAHLISESDNPEDDKVYFFFRENAIDGEH 256

Qy     246 MGKVVFPRVAQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPG----DSHFYFNILQAVTD 301
      || |: |:| || | | :||:| ||||| ||||| |:| : |
Db     257 SGKATHARIGQICKNDFGG-HRSLVNKWTTF LKARLICSVPGPNGIDTHF-----DELQD 310

Qy     302 VIRINGRD----VVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVP 357
      | :| :| || |:| | |||| | | |: || | : : |: | |
Db     311 VFLMNFKDPKNPVVYGVFTTSSNIFKGSAVCMYSMSDVRRVFLGPYAHRDGPYQWVPY- 369

Qy     358 DERVPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVR 417
      ||| |||| | | : : : : ||| : | :|| | | : ||| :| |
Db     370 QGRVPYPRPGTCP-SKTFFGGFDSTKDLPPDVITFARSHPAMYNPVFPMNNRPVIVIKTDVN 428

Qy     418 YRLTKIAVDTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLNDSLFLEEMSVYNSEKC 477
      |: |:| || : |:|:|:| | :|| : : : : | |||:|:
Db     429 YQFTQIVVDRVDAEDGQYDVMFIGTDVGTVLKVVSIPKETWYDLEEV LLEEMTVFR---- 484

Qy     478 SYDGVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGR CERH GKCKKTCIASRDPYCGWIK 537
      | | |:| ||: : | :|| ||: :|| | :| |||| |
Db     485 -----EPTAISAMELSTKQQQLYIGSTAGVAQLPLHRCDIYGKACAECCLARDPYCAW-- 537

Qy     538 EGGACSHLSPNS-RLTFEQDIERGNTDGLGDC----HNSFVALNGHS--SSLLPSTTTSD 590
      :| ||| | : | | ||| | | | | :|: : ||| : : |
Db     538 DGSACSRYPFTAKRRTRRQDIRNG--DPLTHCSDLHHDNH---HGHSPEERIIYGVENSS 592

Qy     591 STAQEGYESRGGMLDWKHL LSPDSTDP LGAVSSSHNHQDKKGVIRE 637
      : : :|: :| : : : : | | : :|:| |
Db     593 TFLECSPKSQRALVYWQFQRRNEERKEEI-RVDDHII RTDQGLLLRS 638

```

RESULT 14

SM1A_TRICF

ID SM1A_TRICF STANDARD; PRT; 712 AA.

AC Q26972;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Semaphorin 1A precursor (Semaphorin-I).

GN SEMA-1A OR TSEMA-I.
 OS Tribolium confusum (Confused flour beetle).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;
 OC Tenebrionidae; Tribolium.
 OX NCBI_TaxID=7071;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RX MEDLINE=94094332; PubMed=8269517;
 RA Kolodkin A.L., Matthes D.J., Goodman C.S.;
 RT "The semaphorin genes encode a family of transmembrane and secreted
 RT growth cone guidance molecules.";
 RL Cell 75:1389-1399(1993).
 CC -!- FUNCTION: PLAY A ROLE IN GROWTH CONES GUIDANCE.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- SIMILARITY: Belongs to the semaphorin family.
 CC -!- SIMILARITY: Contains 1 Sema domain.
 CC -----
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 CC -----
 DR EMBL; L26080; AAA16609.1; -.
 DR InterPro; IPR003659; Plexin-like.
 DR InterPro; IPR002165; Plexin_repeat.
 DR InterPro; IPR001627; Sema.
 DR Pfam; PF01437; PSI; 1.
 DR Pfam; PF01403; Sema; 1.
 DR SMART; SM00423; PSI; 1.
 DR SMART; SM00630; Sema; 1.
 KW Signal; Developmental protein; Transmembrane; Glycoprotein;
 KW Neurogenesis.
 FT SIGNAL 1 20 POTENTIAL.
 FT CHAIN 21 712 SEMAPHORIN 1A.
 FT DOMAIN 21 601 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 602 622 POTENTIAL.
 FT DOMAIN 623 712 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 213 506 SEMA.
 FT DOMAIN 470 473 POLY-VAL.
 FT DOMAIN 612 616 POLY-VAL.
 FT CARBOHYD 42 42 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 69 69 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 161 161 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 265 265 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 712 AA; 79751 MW; C0734FE5B9C09FE3 CRC64;

Query Match 15.5%; Score 845; DB 1; Length 712;
 Best Local Similarity 28.9%; Pred. No. 6.8e-47;
 Matches 230; Conservative 130; Mismatches 270; Indels 166; Gaps 30;

Qy 12 LLHFAGAGFPEDSEPI-----SISHGNYTKQYPVFGHKPGRNTTQRHRLDIQMIMIMN- 65
 |: | |: | : |: ::| | | :||

Db 12 LIALCHAWMPDSSSKLINHFKSVESKSFT-----GNATFPDH-----FIVLNQ 54
 Qy 66 --GTLYIAARDHIYTVDI-DTSHTEEIYCSKKLWKSQRQADVDCRMKGKHKDECHNFIK 122
 : : : | : : | : | : : : : | : | : | : | : | : | :
 Db 55 DETSILVGGRNRVYNLSIFDLSEK----GGRIDWPSSDAHGQLCILKGKTDDDCQNYIR 110
 Qy 123 VLLKKNDALFVCGTNAFNPSCRNYKMDTLEPFGD-EFSGMARCPYDAKHANVALFADGK 181
 : | : | : | : | : | : : : | : | : | : | : | : : : :
 Db 111 ILYSSEPGLVICGTNSYKPLCRTYAFKEGKYLVEKEVEGIGLCPYNPEHNSTSVSYNGQ 170
 Qy 182 LYSATVTDFLAIDAVIYRSLGESPTLRVTKHDSKWLKEPYFVQAVDYGDIYFFFREIAV 241
 | : | | | | | : | : | : | : | : | : | : | : | : | : | :
 Db 171 LFSATVADFSGGDPLIYRE-----PQTELSDLKQLNAPNFVNSVAYGDYIFFFFYRETAV 225
 Qy 242 EYNTMGKVVFPRAVQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDSSHFYFNILQAVTD 301
 | | | : | : | : | : | : : : | : | : | : | : | : | : | :
 Db 226 EYMNCCKVIYSRVARVCKDDKGGPHQSRDR-WTSFLKARLNCSIPGEYPFYFDEIQSTSD 284
 Qy 302 VI--RINGRD---VVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPV 356
 : : | | | : : : | : | : | : | : | : | : | : | : | : | :
 Db 285 IVEGRYNSDDSKKIIYGILTPVNAIGGSAICAYQMADILRVFEGSFKHQETINSNWLVPV 344
 Qy 357 PDERVPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMV 416
 | | : | | | | : : : | : | : | : | : | : | : | : | :
 Db 345 PQNLVPEPRPGQCVRDSRI-----LPDKNVNFIKTHSLMED-VPALFGKPVILVRVSL 395
 Qy 417 RYRLTKIAVDTAAGPYQNH--TVVFLGSEKGIILKFLARIGNSGFLNDSLFLLEEMSVYNS 474
 : | | | | | : | : | : | : | : | : | : | : | : | : | :
 Db 396 QYRFTAITVDPQVKTINNQYLDVLYIGTDDGKVLK----- 430
 Qy 475 EKCSYDGVEDKRIMGMQLDRASSSLYAFSTCV-----IKVP----- 511
 : : : | : | : | : : : : : : : : : : : : : : : :
 Db 431 -----AVNIPKRHAKALLYRKYRTSVHPHGAPVKQLKIAPGYKVVVVGKDEI 478
 Qy 512 ----LGR CERH GKCKKTCIASRDPYCGWIKEGGACSHLSPNSRLTF-EQDIERN----- 561
 | | : | | : : | : | : : | : : : | : | : | : | :
 Db 479 RLANLNHCASKTRC-KDCVELQDPHCAWDAKQNLCSIDTVTSYRFLIQDVVRGDDNKCW 537
 Qy 562 ---TDGLGDCHNSFVALNGHSSSLPSTTTSDSTAQEGYESRGGMLDWKHLLDSPDSTDP 618
 | | | : | : | : | : : | : | : | : | : | : | : | :
 Db 538 SPQTDKKTVIKNK-----PSEVENEIT-----NSIDEKDL----DSSDP 572
 Qy 619 LGAVSSHNHQDKKGVIRESYLKG---HDQLVPVT--LLAIAVILAFVMGA---VFSGITV 670
 | : | : | : | : | : | : | : | : | : | : | : | : | :
 Db 573 LIKTGLDDSDCDPV-SENSIGGCAVRQQLVIYTAGTLHIVVVVVSIVGLFSWLVSGLSV 631
 Qy 671 YCV--CDHRRKDVAVVQRKE--KELTHSRGMS-SVTKLSGLFGDTQSKDPKPEAILTP 725
 : | : : : : : | : : : | : : | : | : | : | : | :
 Db 632 FAKFHSDSQYPEAPFIEQHNHLERLSANQTGYLTPRANKAVNLVVKVSSSTPRPKDNLD 691
 Qy 726 LMHNGKLATPGNTAKM 741
 : : : | : | :
 Db 692 VSKDLNIASDGTLOKI 707

ID SZ1B_BRARE STANDARD; PRT; 778 AA.
 AC Q9W686;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Semaphorin Z1B precursor (Semaphorin 1B) (Sema-Z1B).
 GN SEMAZ1B OR SEMA3AB.
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99425174; PubMed=10495275;
 RA Roos M., Schachner M., Bernhardt R.R.;
 RT "Zebrafish semaphorin Z1b inhibits growing motor axons in vivo."
 RL Mech. Dev. 87:103-117(1999).
 CC -!- FUNCTION: MIGHT NORMALLY INFLUENCE THE MIDSEGMENTAL PATHWAY CHOICE
 CC OF THE VENTRALLY EXTENDING MOTOR AXONS BY CONTRIBUTING TO A
 CC REPULSIVE DOMAIN IN THE POSTERIOR SOMITE.
 CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN RHOMBOMERES THREE AND FIVE, AND
 CC IN THE POSTERIOR HALF OF NEWLY FORMED SOMITES WHICH IS AVOIDED BY
 CC VENTRALLY EXTENDING MOTOR AXONS.
 CC -!- SIMILARITY: Belongs to the semaphorin family.
 CC -!- SIMILARITY: Contains 1 Sema domain.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
 CC -----
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 DR EMBL; AF083382; AAD28103.1; -.
 DR ZFIN; ZDB-GENE-991209-6; sema3ab.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR003659; Plexin-like.
 DR InterPro; IPR002165; Plexin_repeat.
 DR InterPro; IPR001627; Sema.
 DR Pfam; PF00047; ig; 1.
 DR Pfam; PF01437; PSI; 1.
 DR Pfam; PF01403; Sema; 1.
 DR SMART; SM00409; IG; 1.
 DR SMART; SM00423; PSI; 1.
 DR SMART; SM00630; Sema; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW Signal; Immunoglobulin domain; Multigene family; Neurogenesis;
 KW Developmental protein; Glycoprotein.
 FT SIGNAL 1 17 POTENTIAL.
 FT CHAIN 18 778 SEMAPHORIN Z1B.
 FT DOMAIN 241 539 SEMA.
 FT DOMAIN 579 668 IG-LIKE C2-TYPE.

